

# FIG. 1A

1 CACCTATCC TACACTACTA GGAACCTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
121 GCAGCCAAAC GCCTCCTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCCTC CTCCATCCAC 240  
241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
1 M A R A H W G C C P W L 12  
301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
13 V L L C A C A W G H T K P L D L G G Q D 32  
361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
33 V R N C S T N P P Y L P V T V V N T T M 52  
421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAAACATG ACGAGAGGCG TGCCTGGATT 540  
73 G T D A H M N E Y I G Q H D E R R A W I 92  
541 ACAGGCTTTA CAGGGCTCTGC AGGAACGTCA GTGGTACTA TGAAGAAAGC AGCTGTCTGG 600  
93 T G F T G S A G T A V V T M K K A A V W 112  
601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
113 T D S R Y W T Q A E R Q M D C N W E L H 132  
661 AAGGAAGTTG GCACCACTCC TATTGTCACT TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720  
133 K E V G T T P I V T W L L T E I P A G G 152  
721 CGTGTGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
153 R V G F D P F L L S I D T W E S Y D L A 172  
781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840  
173 L Q G S N R Q L V S I T T N L V D L V W 192  
841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900  
193 G S E R P P V P N Q P I Y A L Q E A F T 212  
901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
213 G S T W Q E K V S G V R S Q M Q K H Q K 232

## FIG. 1B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCCTACA CGCTGCTCAC AGACTCTTCT 1080  
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440  
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAATG CTGCCCTGGC CCACTACAGC 1560  
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGGCCCGCAG AGCCTTGTGG 1800  
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
513 D A G L N Y G H G T G H G I G N F L C V 532

# FIG. 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCG GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGCC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

## FIG. 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

## FIG. 2A

1 CACCCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
 181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCG CTCCATCCAC 240  
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
 1 M A R A H W G C C P W L 12  
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
 13 V L L C A C A W G H T K P L D L G G Q D 32  
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGCAA TACCACAATG 420  
 33 V R N C S T N P P Y L P V T V V N T T M 52  
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540  
 73 G T D A H M N E Y I G Q H D E R R A W I 92  
 541 ACAGGCTTTA CAGGGTCTGC AGGAAC TGCA GTGGTACTA TGAAGAAAGC AGCTGTCTGG 600  
 93 T G F T G S A G T A V V T M K K A A V W 112  
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
 113 T D S R Y W T Q A E R Q M D C N W E L H 132  
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720  
 133 K E V G T T P I V T W L L T E I P A G G 152  
 721 CGTGTGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
 153 R V G F D P F L L S I D T W E S Y D L A 172  
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840  
 173 L Q G S N R Q L V S I T T N L V D L V W 192  
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTACACA 900  
 193 G S E R P P V P N Q P I Y A L Q E A F T 212  
 901 GGGAGCACTT GGCAAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

## FIG. 2B

961 GTCCCGACTG CCGTCCTTCT GTGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTCTTC TATTCTACCA CGCTGCTCAC AGACTCTTCT 1080  
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGGGGAC 1380  
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGCTGG CTGGAGAAGA ACCTGCCAA AGGCACAGTG 1440  
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACAA GTTCTCCTCC 1500  
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAATG CTGCCCTGGC CCACTACAGC 1560  
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGAG AGCCTTGTTG 1800  
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
 513 D A G L N Y G H G T G H G I G N F L C V 532

## FIG. 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTGTG GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGAG AAGGTGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCGAGTG GCTTCAACAGCACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCAG GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAAAC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

## FIG. 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTG CAGCTGTTG ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

# FIG. 3A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTCC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 3B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

## FIG. 4A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAACTA CCTGGCCAAC 240  
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420  
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCCGA GGCAGGCCCG GGTACCTGC 480  
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCCA TGAGGCCTGG 600  
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGGAGGAGGT CAGCAGGACA 720  
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840  
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 4B

901 TTCTTGCGCT TCACTAACAG CTCCCTGAAT CCAGTAATTG ATGTCTTGT GGGCCAGCTC 960  
299 F F A F T N S S L N P V I Y V F V G Q L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTCTGGC GGAATTAAGA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

# FIG. 5A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCAA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCGTGC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGGGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACCC GGGAGGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGGCGAACCG TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 5B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGAT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

# FIG. 6A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGCTGTTC GTGAGGACTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 6B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCATTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCTGG GTTTCTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

## FIG. 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTÀ TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTÀ ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCACT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAG TGTGAAAGAG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTÀ GAACCTGGAG AGCCAGAACCC TGGAGGGCTÀ GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGAA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 6D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAAGAA CATCTGTCC 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

# FIG. 7A

1 AATTCAGAGC CACCGGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120  
121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
181 CAGATAGTAG GCTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
1 M D N V L P V D S D 10  
241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
11 L S P N I S T N T S E P N Q F V Q P A W 30  
301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
31 Q I V L W A A A Y T V I V V T S V V G N 50  
361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAACGA GGACAGTGC GAACTATTTT 420  
51 V V V M W I I L A H K R M R T V T N Y F 70  
421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
71 L V N L A F A E A S M A A F N T V V N F 90  
481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCTGTTCT ACTGCAAGTT CCACAACTTC 540  
91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
541 TTTCCCATCG CGCGTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
111 F P I A A V F A S I Y S M T A V A F D R 130  
601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCA CGCACAGCCAC CAAAGTGGTC 660  
131 Y M A I I H P L Q P R L S A T A T K V V 150  
661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTCC CCCAGGGCTA CTACTCAACC 720  
151 I C V I W V L A L L L A F P Q G Y Y S T 170  
721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
171 T E T M P S R V V C M I E W P E H P N K 190  
781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840  
191 I Y E K V Y H I C V T V L I Y F L P L L 210  
841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
211 V I G Y A Y T V V G I T L W A S E I P G 230  
901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
231 D S S D R Y H E Q V S A K R K V V K M M 250

## FIG. 7B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAAATGCTC TTACAGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCCTTGG CAGGTGCAGC CCCCAC TGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

# FIG. 8A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120  
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
 1 M D N V L P V D S D 10  
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300  
 11 L S P N I S T N T S E P N Q F V Q P A W 30  
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
 31 Q I V L W A A A Y T V I V V T S V V G N 50  
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAACATGA GGACAGTGAC GAACTATTTT 420  
 51 V V V M W I I L A H K R M R T V T N Y F 70  
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
 71 L V N L A F A E A S M A A F N T V V N F 90  
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTTC 540  
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
 541 TTCCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
 111 F P I A A V F A S I Y S M T A V A F D R 130  
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCA CCACAGCCAC CAAAGTGGTC 660  
 131 Y M A I I H P L Q P R L S A T A T K V V 150  
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTC CCCAGGGCTA CTACTCAACC 720  
 151 I C V I W V L A L L L A F P Q G Y Y S T 170  
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAAG 780  
 171 T E T M P S R V V C M I E W P E H P N K 190  
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840  
 191 I Y E K V Y H I C V T V L I Y F L P L L 210  
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
 211 V I G Y A Y T V V G I T L W A S E I P G 230  
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
 231 D S S D R Y H E Q V S A K R K V V K M M 250

## FIG. 8B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCCATCA TCTACTGCTG CCTCAATGAC 1140  
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAAATGCTC TTCACGAAAGT 1380  
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
 391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCAC TGACCTGCCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTTC AGGATG 1766

# FIG. 9A

1 AATTCAGAGC CACCGCGGGC AGGCAGGAG TGCATCCAGA AGCGTTATA TTCTGAGCGC 60  
61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTT 120  
121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
181 CAGATAGTAG GCTTACGCC TAGCTCGAA ATGGATAACG TCCTCCCGT GGACTCAGAC 240  
1 M D N V L P V D S D 10  
241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300  
11 L S P N I S T N T S E P N Q F V Q P A W 30  
301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
31 Q I V L W A A A Y T V I V V T S V V G N 50  
361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420  
51 V V V M W I I L A H K R M R T V T N Y F 70  
421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
71 L V N L A F A E A S M A A F N T V V N F 90  
481 ACCTATGCTG TCCACAACGA ATGGTACTAC GCCCTGTTCT ACTGCAAGTT CCACAACCTTC 540  
91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
111 F P I A A V F A S I Y S M T A V A F D R 130  
601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAAG CCACAGCCAC CAAAGTGGTC 660  
131 Y M A I I H P L Q P R L S A T A T K V V 150  
661 ATCTGTGTCA TATGGGTCTT GGCTCTCCTG CTGGCCTTC CCCAGGGCTA CTACTCAACC 720  
151 I C V I W V L A L L L A F P Q G Y Y S T 170  
721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAAG 780  
171 T E T M P S R V V C M I E W P E H P N K 190  
781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840  
191 I Y E K V Y H I C V T V L I Y F L P L L 210  
841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
211 V I G Y A Y T V V G I T L W A S E I P G 230  
901 GACTCCCTCG ACCGCTACCA CGAGCAAGTC TCTGCCAAC GCAAGGTGGT CAAAATGATG 960  
231 D S S D R Y H E Q V S A K R K V V K M M 250

## FIG. 9B

961 ATTGTCTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAAATGCTC TTACAGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCCTTGG CAGGTGCAGC CCCCAC TGACCTGC CTCCCTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

# FIG. 10A

1 AATTCAAGGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60  
 61 CAGTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120  
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
 181 CAGATAGTAG GCTTACGCC TAGCTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240  
 1 M D N V L P V D S D 10  
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
 11 L S P N I S T N T S E P N Q F V Q P A W 30  
 301 CAAATTGTCC TTTGGGCAGC TGCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
 31 Q I V L W A A A Y T V I V V T S V V G N 50  
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420  
 51 V V V M W I I L A H K R M R T V T N Y F 70  
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
 71 L V N L A F A E A S M A A F N T V V N F 90  
 481 ACCTATGCTG TCCACAAACGA ATGGTACTAC GGCTGTTCT ACTGCAAGTT CCACAACCTTC 540  
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
 111 F P I A A V F A S I Y S M T A V A F D R 130  
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAAG CCACAGCCAC CAAAGTGGTC 660  
 131 Y M A I I H P L Q P R L S A T A T K V V 150  
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTC CCCAGGGCTA CTACTCAACC 720  
 151 I C V I W V L A L L L A F P Q G Y Y S T 170  
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAAG 780  
 171 T E T M P S R V V C M I E W P E H P N K 190  
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCCTGCTG 840  
 191 I Y E K V Y H I C V T V L I Y F L P L L 210  
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
 211 V I G Y A Y T V V G I T L W A S E I P G 230  
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960  
 231 D S S D R Y H E Q V S A K R K V V K M M 250

## FIG. 10B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAAATGCTC TTCACGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCCTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAACACACC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCC ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

# FIG. 11A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCTC GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F V E P I L 60  
 241 GAGGTTCCA GCTTGCAGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCAC TG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATT CACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540  
 141 V L G D A L V D F S L K L Y H A F S A M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAACCTGG AGAGCATTCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 11B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTAACCT GTGTGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

# FIG. 12A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
1 M A S R L T L L T L L L L A G D R A 20  
  
121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
21 S S N P N A T S S S S Q D P E S L Q D R 40  
  
181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTGTTGA ACCCATCCTG 240  
41 G E G K V A T T V I S K M L F V E P I L 60  
  
241 GAGGTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
61 E V S S L P T T N S T T N S A T K I T A 80  
  
301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
81 N T T D E P T T Q P T T E P T T Q P T I 100  
  
361 CAACCCACCC AACCAACTAC CCAGCTCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
  
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
121 S F C P G P V T L C S D L E S H S T E A 140  
  
481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
141 V L G D A L V D F S L K L Y H A F S A M 160  
  
541 AAGAAGGTGG AGACCAACAT GGCCTTTCC CCATTAGCA TCGCCAGCCT CCTTACCCAG 600  
161 K K V E T N M A F S P F S I A S L L T Q 180  
  
601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
181 V L L G A G Q N T K T N L E S I L S Y P 200  
  
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
201 K D F T C V H Q A L K G F T T K G V T S 220  
  
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
221 V S Q I F H S P D L A I R D T F V N A S 240  
  
781 CGGACCCGT ACAGCAGCAG CCCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTGGAG 840  
241 R T L Y S S S P R V L S N N S D A N L E 260  
  
841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
261 L I N T W V A K N T N N K I S R L L D S 280  
  
901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAAGTGGAG 960  
281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 12B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTTGA CCAAACATTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTAACCT GTGTGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCA AGACAGTGCT GGAACGTACA GAGACTGGGG TGGAGGGCGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCCAGAC 1800

1801 TCTATAAAATA AAACCTGACA GACCAT 1826

# FIG. 13A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F A E P I L 60  
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCAC TG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCAACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGCAATG 540  
 141 V L G D A L V D F S L K L Y H A F S A M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAACCTGG AGAGCCTCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC ACAACAAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 13B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACTTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGG GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGG ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACGTGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCC CTGACTGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTCT CTAGTTCAAG TTCACCCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

# FIG. 14A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCTC GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GGCAGAGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F V E P I L 60  
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCACGT ATGAACCCAC CACACAACCC ACCACAGAGC CCACCCACCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGGAATG 540  
 141 V L G D A L V D F S L K L Y H A F S G M 160  
 541 AAGAAGGTGG AGACCAACAT GGCCTTTCC CCATTCAAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 14B

961 ACAACATTTG ATCCCAGAA AACCAGAATG GAACCCTTC ACTTCAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATGTA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTCTTATG ACCTAACCT GTGTGGCTG ACAGAGGACC CAGATCTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAACGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500  
461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

# FIG. 15A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTGGAGT CCGCTGACGT CGCCGCCAG 60  
61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
1 M A S R L T L L T L L L L A G D R A 20  
121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
21 S S N P N A T S S S S Q D P E S L Q D R 40  
181 GGCGAAGGGAGGAGTCGCAAC AACAGTTATC TCCAAGATGC TATTGTTGA ACCCATCCTG 240  
41 G E G K V A T T V I S K M L F V E P I L 60  
241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
61 E V S S L P T T N S T T N S A T K I T A 80  
301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360  
81 N T T D E P T T Q P T T E P T T Q P T I 100  
361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
121 S F C P G P V T L C S D L E S H S T E A 140  
481 GTGTTGGGGG ATGCTTTGGT AGATTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540  
141 V L G D A L V D F S L K L Y H A F S A M 160  
541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTCAGCA TCGCCAGCCT CCTTACCCAG 600  
161 K K V E T N M A F S P F S I A S L L T Q 180  
601 GTCCTGCTCG GGGCTGGCA GAACACAAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
181 V L L G A G Q N T K T N L E S I L S Y P 200  
661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
201 K D F T C V H Q A L K G F T T K G V T S 220  
721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
221 V S Q I F H S P D L A I R D T F V N A S 240  
781 CGGACCCGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTGGAG 840  
241 R T L Y S S S P R V L S N N S D A N L E 260  
841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
261 L I N T W V A K N T N N K I S R L L D S 280  
901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAAG 960  
281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 15B

961 ACAACATTTG ATCCCAAGAA AACCGAGAATG GAACCCTTC ACTTCAAAAA CTCAGTTATA 1020  
301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACTTG 1080  
321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAATGGG GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCCGC 1260  
381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAAATGGG ATTCTTCGAT 1320  
401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380  
421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAACGTGACA GAGACTGGGG TGGAGGGCGC TGCAGCCTCC 1440  
441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500  
461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560  
481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

# FIG. 16

1 TCCTCCACCT GCTGGCCCTT GGACACCTCT GTCACCAGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCAGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGGGGCTC TGTACCATT CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGGT ACGACGAAAA CACAGCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTGGTGGAGT TGCCCACCGA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAAA TTTCTCATTT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAA ATCCTGCCTA ATGATGAGTG CAAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

# FIG. 17

1 TCCTCCACCT GCTGGCCCT GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCAGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGGT ACGACGAAAA CACAGCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTC A CATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTGGTGGAGT TGCCCACCGA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAA TTTCTCATT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C E K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCCATC C 871

# FIG. 18

1 TCCTCCACCT GCTGGCCCT GGACACCTCT GTCACCATGT GGTTCCCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8  
  
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTG AGTCCCGGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28  
  
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGGGGCTC TGTACCATT CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48  
  
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68  
  
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88  
  
 301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108  
  
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128  
  
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCTGGAGT TGCCCACCCA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T Q E P E 148  
  
 481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAGCATCG AACAGAGAA TTTCTCATT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168  
  
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCCTGCCTA ATGATGAGTG CAAAAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C K K A 188  
  
 601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208  
  
 661 ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228  
  
 721 TCATGGGCT ACGTCCCTTG TGGCACCCCA AAAAAGCCTT CTGTCGCCGT CAGAGTGCCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248  
  
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262  
  
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

**FIG. 19**

BRB1_MOUSE	MASQ. A <del>S</del> LKLQPSNOSQOAPPNITSCEGAPEAWDLLCRVLP <del>G</del> FVIT <del>T</del> CF <del>F</del> GLLG <del>N</del> LIVLS
BRB1_RAT	MASE. V <del>L</del> LELQPSN <del>R</del> SQ <del>A</del> PANITSCESALEDWDLLYRVLPGFVITICFFGLLG <del>N</del> LIVLS
BRB1_HUMAN	MASSWPPL <del>E</del> LOSSNOSQLFPQNATAC <del>D</del> NAPEAWD <del>L</del> LHRLVLP <del>T</del> F <del>I</del> SICFFGLLG <del>N</del> LIVLL
BRB1_RABBIT	MASQ. C <del>P</del> LELQPSNOSQLAPPNATSCSGAP <del>A</del> W <del>D</del> LLLHR <del>L</del> P <del>T</del> F <del>I</del> A <del>I</del> FTLGLLG <del>N</del> SVLS
BRB1_MOUSE	F <del>F</del> LLP <del>P</del> WR <del>R</del> WW...Q <del>O</del> R <del>R</del> QLT <del>A</del> E <del>I</del> YL <del>A</del> AS <del>D</del> L <del>V</del> F <del>V</del> L <del>G</del> L <del>P</del> W <del>A</del> E <del>N</del> GNRFNWPFGSDL
BRB1_RAT	F <del>F</del> LLP <del>P</del> WR <del>R</del> WW <del>W</del> Q <del>O</del> R <del>R</del> QLT <del>A</del> E <del>I</del> YL <del>A</del> AS <del>D</del> L <del>V</del> F <del>V</del> L <del>G</del> L <del>P</del> W <del>A</del> E <del>N</del> GNRFNWPFG <del>T</del> DL
BRB1_HUMAN	V <del>F</del> LLP.....RRQL <del>I</del> MA <del>E</del> YL <del>A</del> AS <del>D</del> L <del>V</del> F <del>V</del> L <del>G</del> L <del>P</del> W <del>A</del> E <del>N</del> W <del>N</del> Q <del>F</del> NWPFG <del>A</del> L
BRB1_RABBIT	V <del>F</del> LLA.....RRRL <del>S</del> MA <del>E</del> YL <del>A</del> AS <del>D</del> L <del>V</del> F <del>V</del> L <del>G</del> L <del>P</del> W <del>A</del> E <del>N</del> W <del>R</del> Q <del>F</del> DWPFGA <del>A</del> L
BRB1_MOUSE	CRVVSGVIKANLFISI <del>F</del> L <del>V</del> V <del>A</del> ISQDRYR <del>L</del> V <del>Y</del> PM <del>T</del> SWG <del>N</del> RRRRQAQ <del>V</del> T <del>C</del> LLI <del>W</del> VAG <del>G</del> LLS
BRB1_RAT	CRVVSGVIKANLF <del>V</del> S <del>I</del> F <del>L</del> <del>V</del> V <del>A</del> ISQDRYR <del>L</del> V <del>Y</del> PM <del>T</del> SWG <del>Y</del> RRRRQAQ <del>A</del> T <del>C</del> LLI <del>W</del> VAG <del>G</del> LLS
BRB1_HUMAN	CRV <del>V</del> NGVIKANLFISI <del>F</del> L <del>V</del> V <del>A</del> ISQDRYR <del>L</del> V <del>H</del> PMASGR <del>G</del> RRRQA <del>R</del> V <del>T</del> C <del>V</del> LI <del>W</del> VVG <del>G</del> LLS
BRB1_RABBIT	CR <del>V</del> VNGVIKANLFISI <del>F</del> L <del>V</del> V <del>A</del> ISQDRY <del>S</del> V <del>L</del> H <del>P</del> MA <del>S</del> RRGRRRQAQ <del>A</del> T <del>C</del> ALI <del>W</del> VAG <del>G</del> LLS
BRB1_MOUSE	TPTFLLRSV <del>K</del> VVP <del>D</del> LN <del>S</del> AC <del>I</del> LLF <del>P</del> HEAWH <del>F</del> V <del>R</del> M <del>V</del> E <del>L</del> N <del>V</del> L <del>G</del> F <del>L</del> L <del>P</del> LA <del>A</del> IL <del>F</del> N <del>S</del> H <del>I</del> L <del>A</del> SL
BRB1_RAT	IPTFLLRSV <del>K</del> VVP <del>D</del> LN <del>S</del> AC <del>I</del> LLF <del>P</del> HEAWH <del>F</del> A <del>M</del> V <del>E</del> L <del>N</del> V <del>L</del> G <del>F</del> L <del>P</del> V <del>T</del> AI <del>I</del> FFNYH <del>I</del> L <del>A</del> SL
BRB1_HUMAN	IPTFLLRS <del>T</del> AV <del>V</del> P <del>D</del> LN <del>S</del> AC <del>I</del> LL <del>F</del> P <del>HE</del> AWH <del>F</del> A <del>R</del> <del>E</del> V <del>E</del> L <del>N</del> V <del>L</del> G <del>F</del> L <del>P</del> LA <del>A</del> IL <del>F</del> NNYH <del>I</del> L <del>A</del> SL
BRB1_RABBIT	TPTF <del>V</del> LR <del>S</del> V <del>R</del> A <del>V</del> P <del>E</del> LN <del>S</del> AC <del>I</del> LL <del>F</del> P <del>HE</del> AWH <del>W</del> L <del>R</del> M <del>V</del> E <del>L</del> N <del>V</del> L <del>G</del> F <del>L</del> L <del>P</del> LA <del>A</del> IL <del>F</del> NNCH <del>I</del> L <del>A</del> SL
*	
BRB1_MOUSE	RGQKEASRTRCGGP <del>K</del> DSKT <del>M</del> CL <del>I</del> L <del>T</del> L <del>V</del> A <del>S</del> F <del>L</del> V <del>C</del> W <del>A</del> P <del>Y</del> H <del>F</del> F <del>A</del> F <del>L</del> F <del>L</del> V <del>Q</del> V <del>R</del> V <del>I</del> Q <del>D</del> C <del>F</del> W <del>K</del> E <del>L</del>
BRB1_RAT	RGQKEASRTRCGGP <del>K</del> GS <del>K</del> TT <del>C</del> CL <del>I</del> L <del>T</del> L <del>V</del> A <del>S</del> F <del>L</del> V <del>C</del> W <del>C</del> PYH <del>F</del> F <del>A</del> F <del>L</del> F <del>L</del> V <del>Q</del> V <del>R</del> V <del>I</del> Q <del>D</del> C <del>S</del> W <del>K</del> E <del>I</del>
BRB1_HUMAN	RTREEVS <del>R</del> TRVRGPKDS <del>K</del> TT <del>A</del> CL <del>I</del> L <del>T</del> L <del>V</del> A <del>F</del> L <del>V</del> C <del>W</del> A <del>P</del> YH <del>F</del> F <del>A</del> F <del>L</del> F <del>L</del> Q <del>V</del> Q <del>A</del> V <del>R</del> G <del>C</del> F <del>W</del> E <del>D</del> F
BRB1_RABBIT	RRRG <del>E</del> RV <del>P</del> SRCGGPR <del>D</del> SK <del>S</del> T <del>A</del> CL <del>I</del> L <del>T</del> L <del>V</del> A <del>S</del> F <del>L</del> V <del>C</del> W <del>A</del> P <del>Y</del> H <del>F</del> F <del>A</del> F <del>L</del> E <del>C</del> L <del>W</del> Q <del>V</del> H <del>A</del> I <del>G</del> G <del>C</del> F <del>W</del> E <del>E</del> F
*	
BRB1_MOUSE	TDLGLQLANFFAFVNSCLNP <del>I</del> YVFAG LF <del>R</del> TK <del>T</del> V <del>L</del> G <del>T</del> -----
BRB1_RAT	TDLGLQLANFFAFVNSCLNP <del>I</del> YVFAG LL <del>R</del> TK <del>T</del> V <del>L</del> G <del>T</del> -----
BRB1_HUMAN	IDLGLQLANFFAFT <del>T</del> N <del>S</del> LN <del>P</del> IYVFVG LF <del>R</del> TK <del>V</del> W <del>E</del> LYK <del>O</del> C <del>P</del> SLAP <del>H</del> SSSHR <del>K</del> E <del>F</del> Q <del>L</del>
BRB1_RABBIT	TDLGLQLSNFSAFVNSCLNP <del>I</del> YVFVG LF <del>R</del> TK <del>T</del> V <del>W</del> E <del>L</del> C <del>Q</del> C <del>S</del> PR <del>S</del> SLAP <del>M</del> SSSR <del>K</del> E <del>M</del> LWG
BRB1_MOUSE	~~~~~
BRB1_RAT	~~~~~
BRB1_HUMAN	FWRN
BRB1_RABBIT	FWRN

**FIG. 20**

BRB2_MOUSE	~~~~~MPCSWKLLGFISVHE . PMPTAASF <small>G</small> IEMFNVTQVLGSALNGT <small>S</small> KDN . CPDTEW
BRB2_RAT	MDTRSSLCP . KTQAVMAVFW . GPGCHLSTCIEMFNITTOALGSAHNGIFSEVN . CPDTEW
BRB2_RABBIT	~~~~~MLNITSQVLAPALNGSVSQSSGC <small>P</small> NTEW
BRB2_CAVPO	~~~~~MFNITSQV . . SALNATIAQGNSCLD <small>A</small> EW
BRB2_HUMAN	~~~~~MFSPW <small>K</small> ISMFSVREDSVPTTASFSADMLNVTLQ . . GPTLN <small>G</small> TFAQ . SKCPQEVW
BRB2_MOUSE	WSWLNAIQAPFLWVLF <small>I</small> LAALENFVLSVFFLHKNSCTVAEIYLG <small>N</small> AAADLILACGLPF
BRB2_RAT	WSWLNAIQAPFLWVLF <small>I</small> LAALENIFVLSVFC <small>L</small> HK <small>I</small> NCTVAEIYLG <small>N</small> AAADLILACGLPF
BRB2_RABBIT	SGWLNVIQAPFLWVLFVLATLENFVLSVFC <small>L</small> HKSSCTVAEYLG <small>N</small> AAADLILACGLPF
BRB2_CAVPO	WSWLNTIQAPFLWVLFVLALENIFVLSVFFLHKSSCTVAEIYLG <small>N</small> AAADLILAFGLPF
BRB2_HUMAN	LGWLNTIQPPFLWVLFVLATLENIFVLSVFC <small>L</small> HKSSCTVAEIYLG <small>N</small> AAADLILACGLPF
BRB2_MOUSE	WAITIANNFDW <small>F</small> GEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGV <small>R</small>
BRB2_RAT	WAITIANNFDWLFGEVLCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGV <small>R</small>
BRB2_RABBIT	WAITIANNFDWLFGEALCRVVNTMIYMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGV <small>R</small>
BRB2_CAVPO	WAITIANNFDWLFGEVLCR <small>M</small> VNTMIQMNNYSSICFLMLVSIDRYLALVKTMSMGRMRGV <small>R</small>
BRB2_HUMAN	WAITISNNFDWLFGETLCRVVNAIISMNLYSSICFLMLVSIDRYLALVKTMSMGRMRGV <small>R</small>
BRB2_MOUSE	WAKLYSLVIWGCTL <small>L</small> SSPMLVFRTMREYSEEGHNVTA <small>C</small> VIVYPSRSWEVFTNVLLNLVG
BRB2_RAT	WAKLYSLVIW <small>S</small> CTLSSPMLVFRTMKDYRDEEGHNVTA <small>C</small> VIVYPSRSWEVFTNM <small>L</small> NNLVG
BRB2_RABBIT	WAKLYSLVIWGCTLSSPMLVFRTMKDYRDECYNTACIDYPSRSWEVFTNVLLNLVG
BRB2_CAVPO	WAKLYSLVIWGCAALLSSPMLVFRTMKDYRDEGHNVTA <small>C</small> IVYPSLIVWQFTNVLLNLVG
BRB2_HUMAN	WAKLYSLVIWGCTLSSPMLVFRTMKEYSDEGHNVTA <small>C</small> VISYPSLIVWEVFTNM <small>L</small> NNVG
BRB2_MOUSE	FLLPLSVITFCTVRITQVLRNNEMKKFKEVOTERKATVVLVLA <small>V</small> LGLFVWCWMPFQISTFL
BRB2_RAT	FLLPLSITFCTVRIMQVLRNNEMKKFKEVOTEKATVVLVLA <small>V</small> LGLFVWCWEPFQISTFL
BRB2_RABBIT	FLLPLSVITFCTVQI <small>T</small> QVLRNNEMQKFKEIQTERRATVVLVLA <small>V</small> LLLFVWCWLPFQISTFL
BRB2_CAVPO	FLLPLSITFCTVQIMQVLRNNEMQKFKEIQTERRATVVLVLA <small>V</small> LLLFVWCWLPFQIGTFL
BRB2_HUMAN	FLLPLSVITFCTMQIMQVLRNNEMQKFKEIQTERRATVVLVLA <small>V</small> LLLFVWCWLPFQISTFL
BRB2_MOUSE	DTLLRLGVLSGCWDEHAVDVITQISSYIAYNSNSCLNPLVYVIVGKFRKKSREVYR <small>V</small> ICQ
BRB2_RAT	DTLLRLGVLSGCWNERAVDITQISSYIAYNSNSCLNPLVYVIVGKFRKKSREVYR <small>A</small> ACP
BRB2_RABBIT	DTLLKLGVLSSCWDEHVIDVITOQGSEMCYNSNSCLNPLVYVIVGKFRKKSREVYH <small>E</small> CR
BRB2_CAVPO	DTLRLLGFLPGCW.EHVIDITQISSYIAYNSNSCLNPLVYVIVGKFRKKSREVYH <small>E</small> CR
BRB2_HUMAN	DTLHLRGILSSCQDERITDVITQIASMAYNSNSCLNPLVYVIVGKFRKKSWEVYQSVCQ
*	
BRB2_MOUSE	K GCMGEPVQMENSMGTLRTSISVERQIHKLQDWAGK <small>R</small> ~~~~~
BRB2_RAT	K GCMGESVQMENSMGTLRTSISVDRQIHKLQDWAGN <small>R</small> ~~~~~
BRB2_RABBIT	KAGCVALEPVQAESMGTLRTSISVERQIHKLP <small>E</small> WTRSSQ~~~~~
BRB2_CAVPO	S GCVSEPAQSENNSMGT <small>L</small> RTSISVDRQIHKLQDWARSSEGT <small>P</small> PGLL
BRB2_HUMAN	K GCRSEPQOMENSMGTLRTSISVERQIHKLQDWAGS <small>R</small> ~~~~~

# FIG. 21A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCNA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTTTG AGCATCCCCA CATTCTGT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTNTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I X L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCNNG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V X G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGCCCC TTACCACTTC TTTGCCTTCC TGGAAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCGTCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 21B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGTT GGGCCNGCTC 960  
299 F F A F T N S S L N P V I Y V F V G X L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

# FIG. 22A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTATA TTCTGAGCGC 60  
61 CAGTCAGCT TTCAAAAAGA GTGCTGCCA TAAAAAGCCT TCCACCCCTCC TGTCTGCTTT 120  
121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180  
181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGT GGACTCAGAC 240  
1 M D N V L P V D S D 10  
241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTCGTGCA ACCAGCCTGG 300  
11 L S P N I S T N T S E P N Q F V Q P A W 30  
301 CAAATTGTCC TTTGGGCAGC TGCCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360  
31 Q I V L W A A A Y T V I V V T S V V G N 50  
361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420  
51 V V V M W I I L A H K R M R T V T N Y F 70  
421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTTC 480  
71 L V N L A F A E A S M A A F N T V V N F 90  
481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCTGTCT ACTGCAAGTT CCACAACTTC 540  
91 T Y A V H N E W Y Y G L F Y C K F H N F 110  
541 TTNCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600  
111 F P I A A V F A S I Y S M T A V A F D R 130  
601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAAG CCACAGCCAC CAAAGTGGTC 660  
131 Y M A I I H P L Q P R L S A T A T K V V 150  
661 ATCTGTGTCA TNTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720  
151 I C V I W V L A L L L A F P Q G Y Y S T 170  
721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780  
171 T E T M P S R V V C M I E W P E H P N K 190  
781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840  
191 I Y E K V Y H I C V T V L I Y F L P L L 210  
841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900  
211 V I G Y A Y T V V G I T L W A S E I P G 230  
901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAATGATG 960  
231 D S S D R Y H E Q V S A K R K V V K M M 250

## FIG. 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCCTCCTG 1020  
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080  
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140  
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200  
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260  
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320  
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAAAGTGCTC TTACACGAAGT 1380  
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440  
391 D S K T M T E S F S F S S N V L S \* 407

1441 GGGCCTTGG CAGGTGCAGC CCCCAC TGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAACACACC TCACACTGGG ACTTGAAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAAATCT CAATTCTTCC CTATCTTGC 1620

1621 CACCCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACCT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTCCCT CAAGAGCCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTC AGGATG 1766

# FIG. 23A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60  
 61 ATGGCCTCCA GGCTGACCCCT GCTGACCCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120  
 1 M A S R L T L L T L L L L L A G D R A 20  
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180  
 21 S S N P N A T S S S S Q D P E S L Q D R 40  
 181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTGNTGA ACCCATCCTG 240  
 41 G E G K V A T T V I S K M L F X E P I L 60  
 241 GAGGTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300  
 61 E V S S L P T T N S T T N S A T K I T A 80  
 301 AATACCAC TG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360  
 81 N T T D E P T T Q P T T E P T T Q P T I 100  
 361 CAACCCACCC AACCAACTAC CCAGCTCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420  
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120  
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480  
 121 S F C P G P V T L C S D L E S H S T E A 140  
 481 GTGTTGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCCT CTCAGNAATG 540  
 141 V L G D A L V D F S L K L Y H A F S X M 160  
 541 AAGAAGGTGG AGACCAACAT GGCTTTCC CCATTAGCA TCGCCAGCCT CCTTACCCAG 600  
 161 K K V E T N M A F S P F S I A S L L T Q 180  
 601 GTCCTGCTCG GGGCTGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCC 660  
 181 V L L G A G Q N T K T N L E S I L S Y P 200  
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720  
 201 K D F T C V H Q A L K G F T T K G V T S 220  
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780  
 221 V S Q I F H S P D L A I R D T F V N A S 240  
 781 CGGACCTGT ACAGCAGCAG CCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840  
 241 R T L Y S S S P R V L S N N S D A N L E 260  
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900  
 261 L I N T W V A K N T N N K I S R L L D S 280  
 901 CTGCCCTCCG ATACCCGCCT TGTCCCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAAG 960  
 281 L P S D T R L V L L N A I Y L S A K W K 300

## FIG. 23B

961 ACAACATTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020  
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATGTA CCAAACTTG 1080  
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140  
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTCAAG 1200  
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAAAGTGG A GATGTCCAAG TTCCAGGCCA CTCTCCTAAC ACTACCCCGC 1260  
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATGGA ATTCTTCGAT 1320  
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380  
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACCC AGACAGTGCT GGAAGTGACA GAGACTGGGG TGGAGGCCGC TGCAGCCTCC 1440  
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500  
 461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGC GAGTATATGA CCCCAGGGCC 1560  
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCCTGCCT GGACTTGCCC CTGCCACCTC CTGCCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AACCTGACA GACCAT 1826

# FIG. 24

1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCTGGT TCTGTGCCTC 60  
 1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120  
 9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT CAGCACTTTC 180  
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGTGCTCA CAGCTGCTCA TTGCATCAGC 240  
 49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGGT ACGACGAAAA CACAGCCAG 300  
 69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360  
 89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420  
 109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCACCNA GGAACCCGAA 480  
 129 P A D T I T D A V K V V E L P T X E P E 148

481 GTGGGGAGCA CCTGTTGGC TTCCGGCTGG GGCAAGCATCG AACAGAGAA TTTCTCATT 540  
 149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAGCC 600  
 169 P D D L Q C V D L K I L P N D E C X K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660  
 189 H V Q K V T D F M L C V G H L E G G K D 208

661. ACCTGTGTGG GTGATTCAAGG GGGCCCGCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720  
 209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AAAAAGCCTT CTGTCGCCGT CAGAGTGCTG 780  
 229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840  
 249 S Y V K W I E D T I A E N S \* 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

# FIG. 25A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCCGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCACTCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGGGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTGCGCTTCC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCGTCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 25B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \*

1081 CC 1082

# FIG. 26A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCG GGTACACTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTGCGCTTCC TGGAAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGCCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 26B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

# FIG. 27A

1 CTGTGCATGG CATCATCCTG GCCCCCCTCA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAAGTTA ACTGGCCTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCGTCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCGTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I V L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACCGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTGCGCTTCC TGGAAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 27B

901 TTCTTGCGCT TCACTAACAG CTCCCTGAAT CCAGTAATTG ATGTCTTGAT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082.

# FIG. 28A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18  
  
 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38  
  
 121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58  
  
 181 CTGTTGGTCT TCCTCCTGCC CGGGCGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78  
  
 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98  
  
 301 AACAGTTA ACTGGCCTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118  
  
 361 GCCAATTGT TCATCAGCAT CTTCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138  
  
 421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGCGGA GGCAGGCCCG GGTCACTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158  
  
 481 GTGCTCATCT GGGTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178  
  
 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198  
  
 601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218  
  
 661 GTCTTCTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R K E V S R T 238  
  
 721 AGAGTGCAGGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V R G P K D S K T T A L I L T L V V A 258  
  
 781 TTCCCTGGTCT GCTGGGCCCT TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278  
  
 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 28B

901 TTCTTGCGCT TCACTAACAG CTCCCTGAAT CCAGTAATTG ATGTCTTGAT GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

# FIG. 29A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCGTGTT GTGAGGACTC CGTGCCCACC 60  
1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240  
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTCTGGG CCATCACCAT CTCCAACAAC 360  
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGCACTGGC TCTTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720  
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840  
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900  
281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 29B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCATGC 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC T TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGACTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCAATT A TAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT ACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

FIG. 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATT A CGCAGACGT ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTGGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAAC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAAACCTGGA GGGCTAGAAC CTGGAGAACAG AGAAAAATTT ACATGGCAA 3180  
3181 GAGCCCATAA ATCCCTGACCA ATCCAACTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 29D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCC 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

# FIG. 30A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCGTTC GTGAGGAATC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGCCACAA CGTCACCGCT TGTGTCAATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCAATC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 30B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 ATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCTAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCTGG GTTTCTTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCATT A ATAAAGGTT A AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

## FIG. 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATT A CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCACCT GTCATTCCA 2280  
2281 CCACCCCTGAG GCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAGG AATGGCAATG GTGTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 30D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCGAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCCGGAGA AGAGCGGCC C TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

# FIG. 31A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTT GTGAGGACTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGGCCGAG CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTCTGGG CCATCACCAT CTCCAACAAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCACTC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGGCGAAC ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GCCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCACTC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K E G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCTGG GTTTCTTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCATT A ATAAAGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTATGT AACATGAAGT 2040

## FIG. 31C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTG GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAACGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTG ACATGGCAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 31D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAAAA AAA 3733

## FIG. 32A

1	CGCCCAACCCAAGTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTAGTCTA	60
61	GGGAAAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTCCTG	120
1	M S S S S W	6
121	GCTCCTCTCAGCCTTGTTGCTGTAAGTGCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTGGACAAGTTAACACAGCGAAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAAATTATAACACCAATTACTGAAGAGAAATGTCCAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTAAAGGAACAGTCCACACTTGCACAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAAGATCTCACAGTCAAGCTCAGCTGCAGGCTCTCAGCAAATGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTTGGCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGGCCAGTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTGAAGAGATTAACCAATTATGAAACATCTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCTATATCAGTCCAATTGGATGCCCTGCTCATTT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

## FIG. 32B

901	GCTTGGTGATATGTGGGGTAGATTTGGACAAATCTGACTCTTGACAGTTCCCTTG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTGATCTGGTCTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTCTGCAGCCACACCTAACGCATTAAAATCCATTGGTCTCTGTCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTCAAGAACAAATGAAACAGAAATAACTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACCTGTGCCCATGATGAAACATACTGTGACCCCGCATCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTGATATTACACAAGGACCCTTACCAATTCCAGTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTGTCAAGCAGCTAACATGAAGGCCCTCTGCACAAATGTGACATCTCAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

## FIG. 32C

1741	CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAAGAACATTCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTAAAAGTAAAAATCAGATGATTCTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTGAAACCAAGAACATCCTCTTAATTCTTGTAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAATGTGTCTGATATCATTCTAGAACTGAAAGTTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTCCGTCTGAATGACAACAGCCTAGAGTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCTTAACCAGCCCCCTGTTCCATATGGCTGATTGTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAATAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTAGACCTCCTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTCTTGTAGGGTATTTGTTGTATGTAATGTTAATTTCATGG	2580
2581	TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAAACTATGACTCTGTCAGA	2640

## FIG. 32D

2641	AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGGCATCTTCATTGACATTGCTTTC	2700
2701	AGTATTATTTCTGTCTCTGGATTGACTTCTGTTCTGTTCTTAATAAGGATTGTAT	2760
2761	TAGAGTATATTAGGGAAAGTGTGTATTGGTCTCACAGGCTGTCAGGGATAATCTAAAT	2820
2821	GTAAATGTCTGTTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTIG	2880
2881	GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCCTGGAACTGGTGTAGC	2940
2941	TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCATTAAATCCATTGTCAAGGATGA	3000
3001	CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTATTGCCTACAGTGATGTT	3060
3061	GGAATCGATCATGCTTCTCAAGGTGACAGGTCTAAAGAGAGAAGAACAGGAAACAG	3120
3121	GTAGAGGACATTGCTTTTCACTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA	3180
3181	AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTTCTAC	3240
3241	TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACGTGATGTTCACCCCTCTGAAGTGGGT	3300
3301	ACCCAGTCTCTAAATCTTGTATTGCTCACAGTGTGAGCAGTGCTGAGCACAAAG	3360
3361	CAGACACTCAATAATGCTAGATTTACACACTCAAAAAAAAAA	3405

## FIG. 33A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCTGCAAAATTCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTCTGGTGAATTACATTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCCCAAGGACCACTCCCAAAGACTTCTATGTTGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 33B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCCACGAAACCATAG	1284
421	V V D P T K P *	428

## FIG. 34A

1	ATGCATCTTATCGACTACCTGCTCCTCCGTGGTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGCCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGCCATGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAATTCCCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAGATTGTGGATTTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTGCTGGTGAATTACATTACTCAAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCCTCAAGGACCACTCCAAAGACTTTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 34B

841	CCTAACCAAGGCAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCCTTGCGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCCACGAAACCATAG	1284
421	V V D P T K P *	428

# FIG. 35A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGGCTACGCCATGCTTCCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGCGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTGATGGTGCTGGTGAATTACATTACTTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCCCTCAAGGACCACCTCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 35B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTTGCGGAAGAGGAATTTCACAAGAAGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTCCTTGTGGTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTCGACCCCACGAAACCATAG	1284
421	V V D P T K P *	428

## FIG. 36A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTGGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGCCATGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAATT CCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGNGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTACTTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCCTCAAGGACCACTCCCAAAGACTNTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 36B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTCACAAGAACAGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTTGATCTTCCACCGACCCAGAGTGTCCCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTGACCCCCACGAAACCATAG	1284
421	V V D P T K P *	428

# FIG. 37A

1	CGCCCAACCCAAGTCAAAGGCTGATAAGAGAGAAAATCTCATGAGGAGGTTTAGTCTA	60
61	GGGAAAGTCATTCACTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTCCTG	120
1	M S S S S W	6
121	GCTCCTCTCAGCCTTGTTGCTGTAAGCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTGGACAAGTTAACACAGGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAAATTATAACACCAATATTACTGAAGAGAAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M M N N A G	66
301	GGACAAATGGTCTGCCCTTTAAAGGAACAGTCCACACTTGGCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAAGATCTCACAGTCAGCTTCAGCTGCAGGCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTGAATGAAATAATGCCAACAGTTAGACTACAATGAGAGGCTCTGGGCTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGTAGATGGCTATGACTACAGCCGGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTCCTATATCAGTCCAATGGATGCCTCCCTGCTCATT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

## FIG. 37B

901	GCTTGGTGATATGTGGGGTAGATTTGGACAAATCTGACTCTTGACAGTTCCCTTG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTGATCTGTTGGCTTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAAACCTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTCTGCTGCCACACCTAACGATTTAAATCCATTGGTCTCTGTCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTCAAGAAGACAATGAAACAGAAATAACTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTACTACATGTTAGAGAAGTGGAGGTGGATGGCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACCTGTGCCCATGATGAAACATACTGTGACCCCGCATCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTGATATTACACAAGGACCCTTACCAATTCCAGTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAACGACTTGTCAAGCAGCTAACATGAAGGCCCTCTGCACAAATGTGACATCTCAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

FIG. 37C

1741	CTCTACAGAAGCTGGACAGAAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTGAGCCCTTATTACCTGGCTGAAAGACCAGAACAGAACATTCTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTGGAGATAAACATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTAAAAGTAAAAATCAGATGATTCTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGGAGTGGCTAATTGAAACCAAGAACATCCTTTAATTCTTGTAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAACGTGTCTGATATCATTCTAGAACTGAAGTTGAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCCGGAGCCGTATCAATGATGCTTCCGTCGAATGACAACAGCCTAGAGTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTGGACCTCCTAACAGCCCCCTGTTCCATATGGCTGATTGTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGTTGGCATTGTCATCCTGATCTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAATAATCCAGGATTCCAAAACACTGATGATGTTAGACCTCCTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTCCCTCTTGAGGTGATTGTTGTATGTAATGTTAATTGATGG	2580
2581	TATAGAAAATATAAGATGATAAGATATCATTAAATGTCAAACATGACTCTGTTCAAGA	2640

## FIG. 37D

2641	AAAAAAATTGTCCAAAGACAAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC	2700
2701	AGTATTTATTCCTGCTCTGGATTTGACTTCTGTTCTTAATAAGGATTTGTAT	2760
2761	TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTCAAGGATAATCTAAAT	2820
2821	GTAAATGTCGTGAATTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTIG	2880
2881	GATCTTGATGGAATATGGATGGATCACTTGTAAGGCAGTGCGCTGGGAACGGTAGC	2940
2941	TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTCATTAAATCCATTGTCAAGGATGA	3000
3001	CATGCTTCTCACAGTAACTCAGTTCAAGTACTATGGTATTTGCCTACAGTGATGTTT	3060
3061	GGAATCGATCATGCTTCTCAAGGTGACAGGTCTAAAGAGAGAAGAACAG	3120
3121	GTAGAGGACATTGCTTTTCACTTCCAAGGTGCTGATCAACATCTCCCTGACAACACAA	3180
3181	AACTAGAGCCAGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAAACTCATTCTAC	3240
3241	TGTTCTCTAACTGTGGAGTGAATGGAAATTCCAACGTGATGTTCACCCCTCTGAAGTGGGT	3300
3301	ACCCAGTCTCTAAATCTTGTATTTGCTCACAGTGTGAGCAGTGCTGAGCACAAAG	3360
3361	CAGACACTCAATAATGCTAGATTTACACACTCAAAAAAAAAAA	3405

# FIG. 38A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCGTNN GTGAGGNCTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V X E X S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCG TGACAAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCCTCTGGG CCATCACCAT CTCCAACAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCCGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGCCACAA CGTCACCGCT TGTGTCTCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTCTAC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCTAC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 38B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATIC GANGLTAATCA CACAGATCGC CTCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCCACGTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K X G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCAATT AATAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTG CCTTTTATGT AACATGAAGT 2040

## FIG. 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCC 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAACAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAACGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 38D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAA AAA 3733

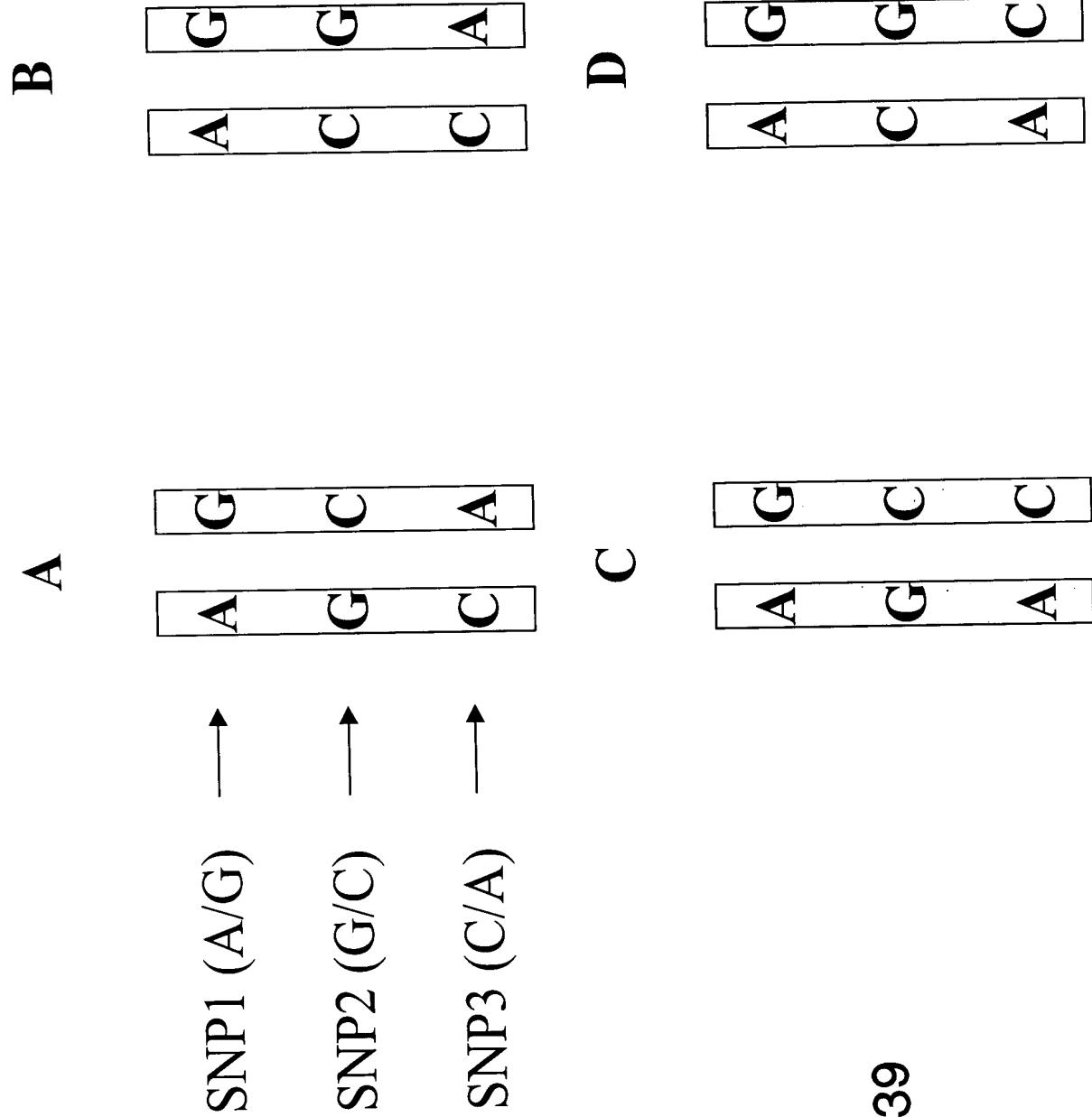
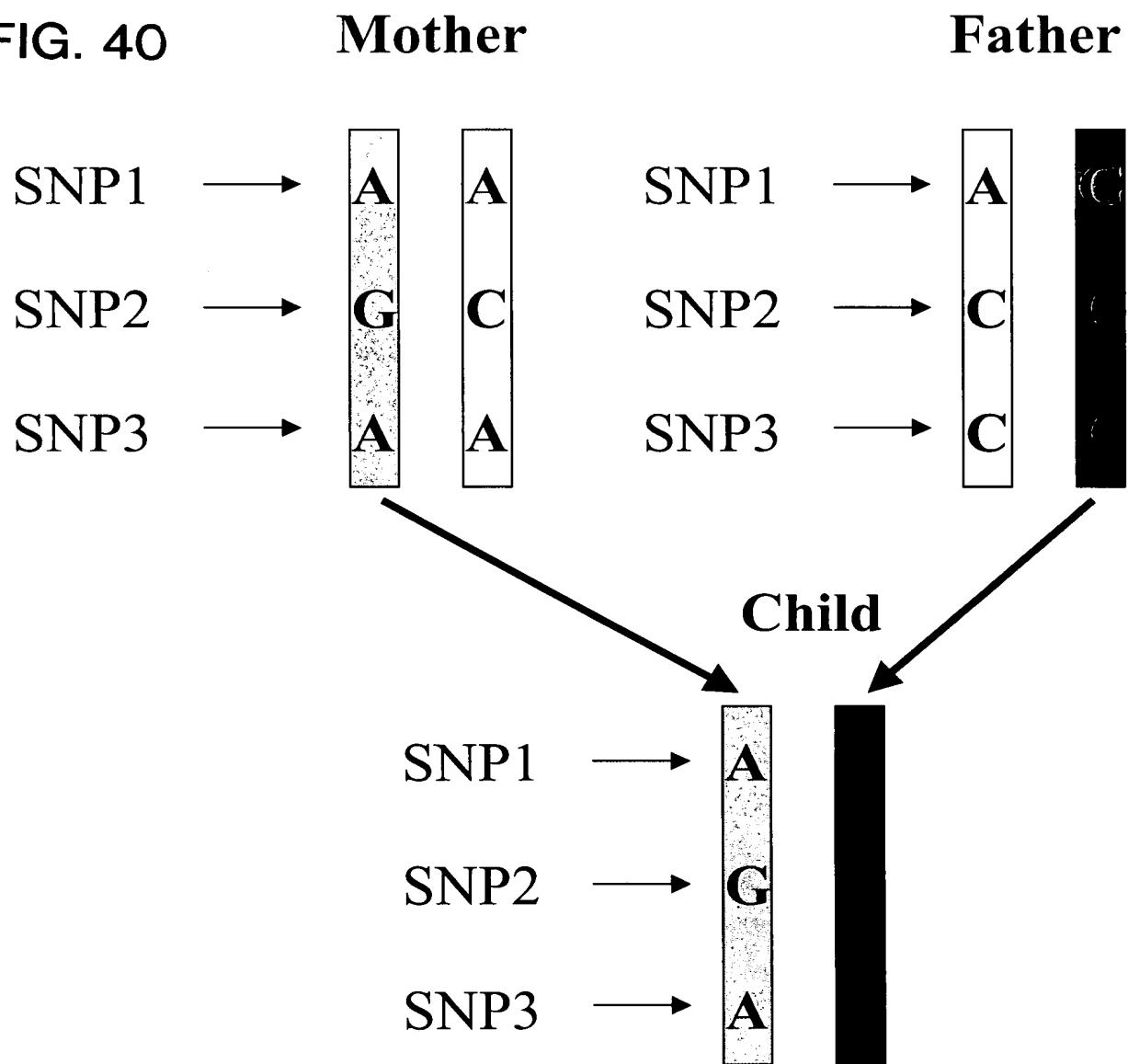


FIG. 39

**FIG. 40**



# FIG. 41A

1 CACCCATATCC TACACTACTA GGAACCTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
 121 GCAGCCAAAC GCCTCCTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
 181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCG CTCCATCCAC 240  
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
 1 M A R A H W G C C P W L 12  
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
 13 V L L C A C A W G H T K P L D L G G Q D 32  
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
 33 V R N C S T N P P Y L P V T V V N T T M 52  
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAAACATG ACGAGAGGCG TGCGTGGATT 540  
 73 G T D A H M N E Y I G Q H D E R R A W I 92  
 541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTACTA TGAAGAAAGC AGCTGTCTGG 600  
 93 T G F T G S A G T A V V T M K K A A V W 112  
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
 113 T D S R Y W T Q A E R Q M D C N W E L H 132  
 661 AAGGAAGTTG GCACCACTCC TATTGTCACT TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720  
 133 K E V G T T P I V T W L L T E I P A G G 152  
 721 CGTGTGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
 153 R V G F D P F L L S I D T W E S Y D L A 172  
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGGA CCTGGTATGG 840  
 173 L Q G S N R Q L V S I T T N L V D L V W 192  
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCAACA 900  
 193 G S E R P P V P N Q P I Y A L Q E A F T 212  
 901 GGGAGCATT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

# FIG. 41B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCCTACA CGCTGCTCAC AGACTCTTCT 1080  
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACCA CCTACTCCCC AGTGATGATG 1320  
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440  
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACCA GTTCTCCTCC 1500  
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560  
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGG CACCCCTCT 1680  
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTTG 1800  
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
 513 D A G L N Y G H G T G H G I G N F L C V 532

# FIG. 41C

1861 CATGAGTGGC CAGTGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGAAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAGCACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCTCA CCCTGCCTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCAGA GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CGGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

## FIG. 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCTTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCGGA ACCCGTCACT ATTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCCA CATTTCCTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428

# FIG. 42A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60  
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120  
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTTGTC 180  
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CGGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240  
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGCAGA GAATATCTGG 300  
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACAGTTA ACTGCCCTT CCGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360  
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGT TCATCAGCAT CTTCCTGGTG GTGCCATCA GCCAGGACCG CTACCGCGTG 420  
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGCCAG CGGAAGGCAG CAGCGCGGA GGCAGGCCCG GGTACACTGC 480  
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCTCTTG AGCATCCCCA CATTCTGCT GCGATCCATC 540  
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600  
 179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660  
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTCTTCA ACTACCACAT CCTGCCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720  
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGG GGCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780  
 239 R V Q G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCT TTACCACTTC TTGCGCTTCC TGGAATTCTT ATTCCAGGTG 840  
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900  
 279 Q A V R G C F W E D F I D L G L Q L A N 298

## FIG. 42B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTGTC GGGCCGGCTC 960  
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020  
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTTCTGGC GGAATTAAAA CAGCATTGAA 1080  
339 S S S H R K E I F Q L F W R N \* 353

1081 CC 1082

## FIG. 43A

1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCCTGTC GTGAGGCCTC CGTGCCCACC 60  
 1 M F S P W K I S M F L S V R E A S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120  
 21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180  
 41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCCTCAGC 240  
 61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGACACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300  
 81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAAC 360  
 101 A A D L I L A C G L P F W A I T I S N N 120

361 TTGACTGGC TCTTGAAA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420  
 121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480  
 141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540  
 161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCCGGAC CATGAAGGAG 600  
 181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660  
 201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTCA CCAACATGCT CCTGAATGTC GTGGCCTTCC TGCTGCCCT GAGTGTCAATC 720  
 221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTCAAG 780  
 241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCAATC 840  
 261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCCTGGATA CGCTGCATCG CCTCGGCATC 900  
 281 I C W L P F Q I S T F L D T L H R L G I 300

## FIG. 43B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCCTTCATG 960  
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGCAA GCGCTTCCGA 1020  
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080  
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140  
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200  
381 H K L Q D W A G S R Q \* 391

1201 AATTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCCAATTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATT A CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCGAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAAGC TAGAACTTTG AAGGACAATT TCTTGCATT A ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGGAGCCAT CTCCATCTTG AAGGAACCTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAAACC ACCTGTCCCT GCCTCAGTT C CTTTATGT AACATGAAGT 2040

## FIG. 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGT AAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100  
2101 GTACATGTGA GGCATCATT ACGCAGACGT ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160  
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220  
2221 AAGCACCAAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280  
2281 CCACCCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT GGAGAGAAGG CCATGTCTTC 2340  
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400  
2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460  
2461 TCAGGGACTG TTCCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520  
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580  
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAAATGA ATATTTATTA GCTGGTTGGA 2640  
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700  
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760  
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820  
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880  
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940  
2941 GAGGGCTAGA ACCTAGAACGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000  
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACCC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060  
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120  
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAACATG AGAAAAAATTT ACATGGCAAA 3180  
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTAAA GCAAAAGCGT GAAAAAAAAG 3240

## FIG. 43D

3241 ATTCCCTCCT TACCCCCAAC CCACTCTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300  
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360  
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAAAG AGGCTGTGTT 3420  
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480  
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540  
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAAGAA CATCTGT CCT 3600  
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660  
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720  
3721 AAAAAAAA AAA 3733

# FIG. 44A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTCGGAGACCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGCCTACGCCATGCTTCCCTGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCGATGTCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGCCATGGGCTGGAAACACGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAAATTCCCTGAATGACACCAG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTACTCAAAGCCCTGTGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCACTTCCCTCAAGGACCACTCCAAAGACTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTTCATGACAGATA	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 44B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTCATAAGAAGCTAGAGTTGCATCTTCCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACGACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCTTGTTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTGACCCCCACGAAACCATAG	1284
421	V V D P T K P *	428

## FIG. 45A

1	ATGCATCTTATCGACTACCTGCTCCTCCCTGGTGGACTACTGGCCCTTCATGGC	60
1	M H L I D Y L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATA GCCCCTGCCAATGCTGACTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTCGGAGACCCCCGGGAAGAACATCTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGCGGCCCTACGCCATGCTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGCCCTGGCTTCAACCTCACCGAGCTGTCTGAGTCGATGCCATAGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGCCATGGGCTGGAAACATGCGTGGC	420
121	F Q H L L H T L N L P G H G L E T C V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCCTGCAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTACTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCCTCAAGGACCACTCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAAGGAGCATCACTGGTATCTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

## FIG. 45B

841	CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG	900
281	P N Q G K M R E I E E V L T P E M L M R	300
901	TGGAACAACTTGTGCGGAAGAGGAATTTACAAGAACGCTAGAGTTGCATCTTCCAAG	960
301	W N N L L R K R N F Y K K L E L H L P K	320
961	TTCTCCATTCTGGCTCCTATGTATTAGATCAGATTTGCCAGGCTGGCTTCACGGAT	1020
321	F S I S G S Y V L D Q I L P R L G F T D	340
1021	CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAACTGGAGGCATCC	1080
341	L F S K W A D L S G I T K Q Q K L E A S	360
1081	AAAAGTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC	1140
361	K S F H K A T L D V D E A G T E A A A A	380
1141	ACCACGTTCGCGATCAAATTCTTCTCTGCCAGACCAATGCCACATCCTGCGATTCAAC	1200
381	T T F A I K F F S A Q T N R H I L R F N	400
1201	CGGCCCTTCCTTGTTGATCTTCCACCAGCACCCAGAGTGTCCCTTTCTGGGCAAG	1260
401	R P F L V V I F S T S T Q S V L F L G K	420
1261	GTCGTGACCCCACGAAACCATAG	1284
421	V V D P T K P *	428

# FIG. 46A

1 CACCCCTATCC TACACTACTA GGAACTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60  
 61 TGCCCACCCCT GGCTCCAAA ACCCTCCAAA ACAAAAGACC AGAAAAGCAC TCTCCACCCA 120  
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCCTC TGTCTGCTCG AGCCCAGGAA 180  
 181 AGGCCTGAAG GAACAGGCCG GGGAAAGGAGC CCTCCCTCTC TCCCTTGTCCT CCATCCAC 240  
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300  
 1 M A R A H W G C C P W L 12  
 301 GTCCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAAGCCAC TGGACCTTGG AGGGCAGGAT 360  
 13 V L L C A C A W G H T K P L D L G G Q D 32  
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420  
 33 V R N C S T N P P Y L P V T V V N T T M 52  
 421 TCACTCACAG CCCTCCGCCA GCAGATGCCAG ACCCAGAACATC TCTCAGCCTA CATCATCCCA 480  
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72  
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCAACATG ACGAGAGGCG TGGTGGATT 540  
 73 G T D A H M N E Y I G Q H D E R R A W I 92  
 541 ACAGGCTTTA CAGGGTCTGC AGGAACGTCA GTGGTGAATC TGAAGAAAGC AGCTGTCTGG 600  
 93 T G F T G S A G T A V V T M K K A A V W 112  
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660  
 113 T D S R Y W T Q A E R Q M D C N W E L H 132  
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720  
 133 K E V G T T P I V T W L L T E I P A G G 152  
 721 CGTGTGGTT TTGACCCCTT CCTCTTGTCC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780  
 153 R V G F D P F L L S I D T W E S Y D L A 172  
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAAACCA ATCTTGTGGA CCTGGTATGG 840  
 173 L Q G S N R Q L V S I T T N L V D L V W 192  
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTATG CCCTGCAGGA GGCATTACAA 900  
 193 G S E R P P V P N Q P I Y A L Q E A F T 212  
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960  
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

## FIG. 46B

961 GTCCCGACTG CCGTCCTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020  
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCTTACA CGCTGCTCAC AGACTCTTCT 1080  
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140  
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCG TGACAGCATC 1200  
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260  
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320  
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAACGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCAGGAC 1380  
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCAA AGGCACAGTG 1440  
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAAC A GTCTCCTCC 1500  
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTGAATG CTGCCCTGGC CCACTACAGC 1560  
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620  
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680  
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740  
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800  
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860  
 513 D A G L N Y G H G T G H G I G N F L C V 532

# FIG. 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAAGGG CATGTTCACT 1920  
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTGGGA TCCGTCTCGA AGATGTGGCT 1980  
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040  
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100  
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160  
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTCGAGTG GCTTCAACAGCACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220  
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280  
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACCTCCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340  
 673 V \*

2341 GCTCCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCC GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCCG GGGTTGTATA CCACACCCCTG 2520

2521 GGCCCCTAAT CCCAGGCCAGA GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACCC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAT CAACCCCCGA CATGGAACCC ATGATTCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTGGC TGTGGAGTAA 2940

## FIG. 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000  
3001 GGCAGCCCGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060  
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCCA CATTCTTGG ATGCCCTTC 3120  
3121 ACCTTGTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAATG AGCTTCAGAC 3180  
3181 AGGGGGTGGG CTTCGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240  
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCCA 3300  
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360  
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTAAA ACAGCCTAAC AAAGACACTT 3420  
3421 GCCTGTGG 3428



**Table III**

Gene Name	Coriell DNA Panel(s)	Amplicon No.	Total SNPs	Missense	Silent	UTR	Intronic
Aminopeptidase P (XPNPEP2)	24 + 47 (55AA) +12pt	24	30	0	2	7	21
Bradykinin B1 receptor (BDKRB1)	24+ 95 (8AA, 103 CAU) +12pt	7	14	2	5	3	4
Bradykinin B2 receptor (BDKRB2)	24 (8AA) +12pt	12	36	3	2	14	17
NK1 tachykinin receptor (TACR1)	24 (8AA) +12pt	7	9	0	3	3	3
C1 esterase inhibitor (C1NH)	24 (8AA) +12pt	10	6	2	2	0	2
Kallikrein 1 (KLK1)	7 (7AA) +12pt	5	6	1	1	2	2
Protease Inhibitor 4 (PI4)	7 (7AA) +12pt	8	12	1	3	1	7
Angiotensin Converting Enzyme 2 (ACE2)	7 (7AA) +12pt	20	9	0	0	0	9
<b>Totals:</b>		122	9	18	30	65	

Table IV (1 of 2)

Table IV (2 of 2)

Table V (1 of 2)

Table V (2 of 2)

**Table VI**

GENE DESCRIPTION	HGNC ID	SNP ID	CONTIG NUM	CONTING POS	REF_AA	ALT_AA	EXON	MUTATION_TYPE	REVCMP	REF_CODON	ALT_CODON	PROTEIN_ID	PROTEIN_POS	PROTEIN_SEQ_REF (SEQ ID NO.)	FLANK_SEQ_ALT (SEQ ID NO.)	FLANK_SEQ_REF (SEQ ID NO.)	FLANK_SEQ_ALT (SEQ ID NO.)	REFSEQ_FLANK_REF (SEQ ID NO.)
Aminopeptidase P (membrane-bound)	XPNPFEP2	AE10051	1	127	P	P	Exon20	Silent	0	CCC	CCC	ALB0634_1	607	4	37	100	100	103
Bradykinin Receptor B1	BDKRB1	AE10351	6	307	R	Q	Exon2	Misense	0	CAG	CAG	NP_000701_1	317	6	60	60	123	106
Bradykinin Receptor B1	BDKRB1	AE10352	4	273	P	P	Exon2	Silent	0	CCG	CCG	NP_000701_1	41	10	61	61	124	107
Tachykinin Receptor 1	TACR1	AE10851	1	614	F	F	Exon1	Silent	1	TTT	TTC	NP_001043_1	111	16	61	61	144	207
Tachykinin Receptor 1	TACR1	AE10852	2	789	I	I	Exon2	Silent	1	ATC	ATA	NP_001043_1	154	18	82	82	145	208
Tachykinin Receptor 1	TACR1	AE10857	6	511	S	S	Exon5	Silent	1	TCA	TCA	NP_001043_1	379	20	87	87	150	213
C1 Esterase Inhibitor	C1NH	AE10553	5	368	S	S	Exon7	Silent	0	AGC	AGT	NP_000053_1	406	24	90	90	153	218
C1 Esterase Inhibitor	C1NH	AE10554	7	568	V	A	Exon3	Misense	0	GTT	GCT	NP_000053_1	56	26	91	91	154	217
C1 Esterase Inhibitor	C1NH	AE10555	7	897	A	G	Exon3	Misense	0	GCA	GCA	NP_000053_1	159	28	92	92	155	218
C1 Esterase Inhibitor	C1NH	AE10556	8	276	V	M	Exon8	Misense	0	GTG	ATG	NP_000053_1	480	30	93	93	156	219
Kallikrein 1 (matriptase/ukinase)	KLK1	AE10761	1	153	K	E	Exon4	Misense	0	AAA	AAA	NP_002248_1	186	34	94	94	157	220
Kallikrein 1 (matriptase/ukinase)	KLK1	AE10763	2	805	E	O	Exon3	Misense	0	GAG	GAG	NP_002248_1	145	36	96	96	159	222
Bradykinin Receptor B1	BDKRB1	AE10266	1	67	N	N	Exon3	Silent	0	AAC	AAT	NP_000701_1	114	556	579	579	611	643
Bradykinin Receptor B1	BDKRB1	AE10327	1	181	R	R	Exon3	Silent	0	AGG	AGA	NP_000701_1	152	558	590	590	612	644
Bradykinin Receptor B1	BDKRB1	AE10358	1	266	L	V	Exon3	Misense	0	CTG	CTG	NP_000701_1	191	560	561	561	613	645
Bradykinin Receptor B1	BDKRB1	AE10359	2	136	E	E	Exon3	Silent	0	GAG	GAA	NP_000701_1	233	562	592	592	614	646
Bradykinin Receptor B2	BDKRB2	AE10459	7	339	R	C	Exon2	Misense	1	CCT	TGT	NP_000814_1	14	564	584	584	616	648
Bradykinin Receptor B2	BDKRB2	AE10462	4	918	D	D	Exon3	Silent	1	GAT	GAC	NP_000814_1	311	566	599	599	621	653
Bradykinin Receptor B2	BDKRB2	AE10465	4	1046	G	E	Exon3	Misense	1	GGG	GAG	NP_000814_1	354	568	590	590	622	654
Angiotensin Converting Enzyme 2	ACE2	AE10987	15	241	N	N	Exon16	Silent	1	AAT	AAC	AAFT8220_1	690	843	861	861	633	665
Protease inhibitor 4	P14	AE11062	2	526	F	F	Exon2	Silent	0	TTC	TTT	NP_008203_1	233	574	603	603	635	667
Protease inhibitor 4	P14	AE11065	4	563	S	S	Exon1	Silent	0	AGT	AGC	NP_008203_1	199	576	606	606	638	670

Table VIIA

**Table VII B**

DNA panel	Cortex Catalog #	Sample Description	XPNPEP2	BDKRB1	C1NH	KLK1	P14	ACE2
HD50 AA panel	14537	African American	x					
HD50 AA panel	14583	African American	x					
HD 50 AA panel	14681	African American	x					
HD50 AA panel	14687	African American	x					
HD50 AA panel	14697	African American	x					
HD50 AA panel	14699	African American	x					
HD 50 AA panel	14720	African American	x					
HD50 AA panel	14746	African American	x					
HD 50 AA panel	14754	African American	x					
HD50 AA panel	14755	African American	x					
HD 50 AA panel	14771	African American	x					
HD50 AA panel	14772	African American	x					
HD 50 AA panel	14783	African American	x					
HD50 AA panel	14826	African American	x					
HD 50 AA panel	14837	African American	x					
HD50 AA panel	14862	African American	x					
HD 50 AA panel	14863	African American	x					
HD50 AA panel	14864	African American	x					
HD 50 AA panel	14892	African American	x					
HD50 AA panel	14893	African American	x					
HD 50 AA panel	14894	African American	x					
HD50 AA panel	14895	African American	x					
HD 50 AA panel	14897	African American	x					
HD50 AA panel	14900	African American	x					
HD 50 AA panel	14901	African American	x					
HD50 AA panel	14903	African American	x					
HD 50 AA panel	14904	African American	x					
HD50 AA panel	14905	African American	x					
HD 50 AA panel	14922	African American	x					
HD50 AA panel	14923	African American	x					
HD 50 AA panel	14924	African American	x					
HD50 AA panel	14925	African American	x					
HD 50 AA panel	14932	African American	x					
HD50 AA panel	14933	African American	x					
HD 100 CAU panel	NA 17201	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17202	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17203	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17204	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17205	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17206	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17207	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17208	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17209	Caucasian	x	x	x	x	x	x
HD 100 CAU panel	17210	Caucasian	x	x	x	x	x	x

Table VII

**Table VIIID**

DNA panel	Coriell Catalog #	Sample Description	XPNPEP2	BDKRB1	TACR1	C1NH	KLK1	P14	ACE2
HD 100 CAU panel	17255	Caucasian	x	x					
HD 100 CAU panel	17256	Caucasian	x	x					
HD 100 CAU panel	17257	Caucasian	x	x					
HD 100 CAU panel	17258	Caucasian	x	x					
HD 100 CAU panel	17259	Caucasian	x	x					
HD 100 CAU panel	17260	Caucasian	x	x					
HD 100 CAU panel	17261	Caucasian	x	x					
HD 100 CAU panel	17262	Caucasian	x	x					
HD 100 CAU panel	17263	Caucasian	x	x					
HD 100 CAU panel	17264	Caucasian	x	x					
HD 100 CAU panel	17265	Caucasian	x	x					
HD 100 CAU panel	17266	Caucasian	x	x					
HD 100 CAU panel	17267	Caucasian	x	x					
HD 100 CAU panel	17268	Caucasian	x	x					
HD 100 CAU panel	17269	Caucasian	x	x					
HD 100 CAU panel	17270	Caucasian	x	x					
HD 100 CAU panel	17271	Caucasian	x	x					
HD 100 CAU panel	17272	Caucasian	x	x					
HD 100 CAU panel	17273	Caucasian	x	x					
HD 100 CAU panel	17274	Caucasian	x	x					
HD 100 CAU panel	17275	Caucasian	x	x					
HD 100 CAU panel	17276	Caucasian	x	x					
HD 100 CAU panel	17277	Caucasian	x	x					
HD 100 CAU panel	17278	Caucasian	x	x					
HD 100 CAU panel	17279	Caucasian	x	x					
HD 100 CAU panel	17280	Caucasian	x	x					
HD 100 CAU panel	17281	Caucasian	x	x					
HD 100 CAU panel	17282	Caucasian	x	x					
HD 100 CAU panel	17283	Caucasian	x	x					
HD 100 CAU panel	17284	Caucasian	x	x					
HD 100 CAU panel	17285	Caucasian	x	x					
HD 100 CAU panel	17286	Caucasian	x	x					
HD 100 CAU panel	17287	Caucasian	x	x					
HD 100 CAU panel	17288	Caucasian	x	x					
HD 100 CAU panel	17289	Caucasian	x	x					
HD 100 CAU panel	17290	Caucasian	x	x					
HD 100 CAU panel	17291	Caucasian	x	x					
HD 100 CAU panel	17292	Caucasian	x	x					
HD 100 CAU panel	17293	Caucasian	x	x					
HD 100 CAU panel	17294	Caucasian	x	x					
HD 100 CAU panel	17295	Caucasian	x	x					

Omapatrilat Trial Samples 12 angioedema patients

Table VIII(1 of 2)

Gene Description	HGNC ID	SNP ID	Exon	REVCOMP	PCR Amplon Name	Target Name	PCR Left primer (SEQ ID No:)	PCR Right primer (SEQ ID No:)
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10051	Exon20	0	XPNPEP2_X20a	AGTGTCTTCCTCCCTC	287	TATTCATCTCCCTCCCTC
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10052	Intron3	0	XPNPEP2_X3a	CAGCCAGGACATTAATCA	288	TCTCTACTCCCTCCCTC
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10053	Intron15	0	XPNPEP2_X13a	TAGGGTCTCTCTCTGC	289	A-TAGGATGAGGCTCACGTTGG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10054	Intron15	0	XPNPEP2_X13a	TAGGGTCTCTCTCTGC	300	A-TAGGATGAGGCTCACGTTGG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10055	Intron17	0	XPNPEP2_X12	TGATGAGACCAGCTGTG	301	ACAGAAAAGAACATGGG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10056	Intron7	0	XPNPEP2_X7a	CCAGCTGSSCATACATG	302	GGAGCTGAAATCTGATT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10057	Intron7	0	XPNPEP2_X10a	CCAGCTGSSCATACATG	303	GGAGCTGAAATCTGATT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10058	Intron10	0	XPNPEP2_X10a	CTTCCTTGACCTCCAGAAC	304	CCTGTTTCTCTGGCTCT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10059	Intron10	0	XPNPEP2_X10a	CTTCCTTGACCTCCAGAAC	305	CCTGTTTCTCTGGCTCT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10060	Intron7	0	XPNPEP2_X7a	CCAGCTGSSCATACATG	306	GGAGCTGAAATCTGATT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10061	Intron13	0	XPNPEP2_X13a	TAATAACGGGAGGGTGTG	307	CAGGCTCAGGCTTTCATT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10062	Intron13	0	XPNPEP2_X13a	TAATAACGGGAGGGTGTG	308	CAGGCTCAGGCTTTCATT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10063	Intron13	0	XPNPEP2_X13a	TAATAACGGGAGGGTGTG	309	ACAGAAAAGAACATGGG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10064	Exon1	0	XPNPEP2_X13a	TGATGAGACCAGCTGTG	310	ACAGAAAAGAACATGGG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10065	Exon1	0	XPNPEP2_X13a	GGACATGCTTAAAGATGAC	312	TGAGGGTCTACCTTGTCTT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10066	Intron18	0	XPNPEP2_X30	CGAGCTGSSCATCCACTAC	313	CTGTCGECATCCCTACTAC
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10067	Intron17	0	XPNPEP2_X13a	CCGCTCTTAAAGACACATC	314	CCGCTCTTAAAGACACATC
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10068	Intron17	0	XPNPEP2_X13a	TAATGAGGGCTTCTCTCTG	315	ATAGGATGAGGCTCAGCTG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10069	Intron13	0	XPNPEP2_X13a	TAATGAGGGCTTCTCTCTG	316	ATAGGATGAGGCTCAGCTG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10070	Intron21	0	XPNPEP2_X13a	GGAGCTGSSCATACATG	317	CAAGAAASCCCTGTTCTCTG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10071	Exon21	0	XPNPEP2_X13a	GGAGCTGSSCATACATG	318	TAAGGATGAGGGTACATG
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10072	Intron22	0	XPNPEP2_X22	GAGGCTCCAGACCTCTGTG	319	TAGGAAGCCAGGCTCTGGT
Aminopeptidase P (membrane-bound)	XPNPEP2	AE_10073	Intron21	0	XPNPEP2_X12a	GAGGCTCCAGACCTCTGTG	320	AAGAAAGCCAGGCTCTGGT
Bradykinin Receptor B1	BDKRB1	AE_10074	Exon2	0	XPNPEP2_X13a	CACCCAGGAGAAGTGG	321	CACCCAGGAGAAGTGG
Bradykinin Receptor B1	BDKRB1	AE_10075	Exon2	0	XPNPEP2_X13a	TGCTGCTGCCCCATTAATCT	322	GGAGGCGAGATTCCTAAT
Bradykinin Receptor B1	BDKRB1	AE_10076	Exon1	0	XPNPEP2_X13a	ATCTCTAGTCTCTGGAGGCC	323	ATCTCTAGTCTCTGGAGGCC
Bradykinin Receptor B1	BDKRB1	AE_10077	Exon3	0	XPNPEP2_X13a	GCTGGCTGTTCTGTTCTCTG	324	CCTGGCTGTTCTGTTCTCTG
Bradykinin Receptor B2	BDKRB2	AE_10078	Intron1	1	BDKRB2_X11a	ACTTCCGAACTCAGGSEATC	325	CTTGGTGTGCAAGAAATGC
Bradykinin Receptor B2	BDKRB2	AE_10079	Intron1	1	BDKRB2_X11a	CGACTTAGGCTCTCACCAACA	326	CTTGGTGTGCAAGAAATGC
Bradykinin Receptor B2	BDKRB2	AE_10080	Intron1	1	BDKRB2_X11a	CGAGGCAAAATTACACTTCAA	327	CCGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10081	Intron1	1	BDKRB2_X11a	GGAGGCAAAATTACACTTCAA	328	CCGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10082	Intron1	1	BDKRB2_X11a	GCTCCAGGAGAAGCTGTT	329	CCGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10083	Intron1	1	BDKRB2_X11a	GCAGGCAAAATTACACTTCAA	330	CCGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10084	Intron1	1	BDKRB2_X11a	GCTCCAGGAGAAGCTGTT	331	ATACACACGCTTCCCAGTT
Bradykinin Receptor B2	BDKRB2	AE_10085	Intron1	1	BDKRB2_X11a	CGAGGCAAAATTACACTTCAA	332	CGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10086	Intron2	1	BDKRB2_X11a	CGAGGCAAAATTACACTTCAA	333	CGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10087	Exon3	1	BDKRB2_X11a	GCTCCAGGAGAAGCTGTT	334	CGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10088	Exon3	1	BDKRB2_X11a	GCTCCAGGAGAAGCTGTT	335	CGAGGCAAAATTACACTTCAA
Bradykinin Receptor B2	BDKRB2	AE_10089	Exon3	1	BDKRB2_X11a	TCTCATGCGAGAAGCTGTT	336	CGACTCTCTGCTCCCTA
Bradykinin Receptor B2	BDKRB2	AE_10090	Exon3	1	BDKRB2_X11a	TCTCATGCGAGAAGCTGTT	337	CCACCTCTGCTCCCTA
Bradykinin Receptor B2	BDKRB2	AE_10091	Exon3	1	BDKRB2_X11a	TCTCATGCGAGAAGCTGTT	338	TATGAGCTTACGAGGCTCC
Bradykinin Receptor B2	BDKRB2	AE_10092	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	339	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10093	Exon3	1	BDKRB2_X11a	GCTGAGGAGGCTTACATGAGT	340	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10094	Exon3	1	BDKRB2_X11a	GCTGAGGAGGCTTACATGAGT	341	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10095	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	342	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10096	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	343	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10097	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	344	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10098	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	345	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10099	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	346	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10100	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	347	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10101	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	348	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10102	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	349	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10103	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	350	ACACCTTAAAGCTCCCTT
Bradykinin Receptor B2	BDKRB2	AE_10104	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	351	AGTATGGCTGGTGGTGG
Bradykinin Receptor B2	BDKRB2	AE_10105	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	352	TGATGAGCTTACATGAGT
Bradykinin Receptor B2	BDKRB2	AE_10106	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	353	GTGGATACGAACTGGT
Bradykinin Receptor B2	BDKRB2	AE_10107	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	354	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10108	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	355	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10109	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	356	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10110	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	357	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10111	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	358	CGTCAAGTCAAGTCTGAGT
Bradykinin Receptor B2	BDKRB2	AE_10112	Exon3	1	BDKRB2_X11a	CGTCAAGTCAAGTCTGAGT	359	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10055	Exon5	1	TACR1_X11a	TGATGAGCTTACATGAGT	360	TGATGAGCTTACATGAGT
C1 Esterase Inhibitor	C1INH	AE_10056	Exon3	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	361	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10057	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	362	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10058	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	363	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10059	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	364	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10060	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	365	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10061	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	366	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10062	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	367	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10063	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	368	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10064	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	369	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10065	Exon3	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	370	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10066	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	371	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10067	Exon5	1	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	372	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10068	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	373	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10069	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	374	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10070	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	375	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10071	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	376	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10072	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	377	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10073	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	378	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10074	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	379	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10075	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	380	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10076	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	381	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10077	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	382	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10078	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	383	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10079	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	384	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10080	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	385	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10081	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	386	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10082	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	387	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10083	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	388	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10084	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	389	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10085	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	390	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10086	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	391	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10087	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	392	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10088	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	393	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10089	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	394	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10090	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	395	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10091	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	396	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10092	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	397	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10093	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	398	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10094	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	399	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10095	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	400	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10096	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	401	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10097	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	402	CGTCAAGTCAAGTCTGAGT
C1 Esterase Inhibitor	C1INH	AE_10098	Exon4	0	TACR1_X11a	CGTCAAGTCAAGTCTGAGT	403	CGTCAAGTCAAGTCTGAG

Table VII(2 of 2)

Table IX (1 of 2)

GENE DESCRIPTION	HuNC ID	SNP ID	EXON	REVCOMP	Target Name	Forward sequencing primer	forward seq name	Forward sequencing primer (Seq ID No.)	Reverse sequencing primer (Seq ID No.)	reverse seq name	Reverse sequencing primer (Seq ID No.)
Aminopeptidase P (membrane bound)	XPNPEP2	AE10051	Exon20	0	XPNPEP2-X20a	AAGTCCTCCCTCCCTCACT	AE10051	423	AGCGTGGCTGACTGAAAGT	AE100512	486
Aminopeptidase P (membrane bound)	XPNPEP2	AE10052	Intron3	0	XPNPEP2-X15a	CAGTAATCTAAGTCACGCC	AE10052	424	TGTAGTGCGCTAAATACTCC	AE100520	489
Aminopeptidase P (membrane bound)	XPNPEP2	AE10053	Intron15	0	XPNPEP2-X15a	CACCTTGAAAGCACACGA	AE10053	425	TGTAGTGCGCTAAATACTCC	AE100520	489
Aminopeptidase P (membrane bound)	XPNPEP2	AE10054	Intron15	0	XPNPEP2-X15a	CCCTGCTCAGATCTTGA	AE10054	426	AGAGTGAGAGTGCGCTAAATACTCC	AE100520	490
Aminopeptidase P (membrane bound)	XPNPEP2	AE10055	Intron1	0	XPNPEP2-X15a	GCAAAAGGAAACAGAGATTAAC	AE10055	427	TAACACAGCATCCAGATTAAC	AE100520	491
Aminopeptidase P (membrane bound)	XPNPEP2	AE10056	Intron17	0	XPNPEP2-X15a	AE10056	428	TAACACAGCATCCAGATTAAC	AE100520	492	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10057	Intron17	0	XPNPEP2-X15a	AE10057	429	TAACACAGCATCCAGATTAAC	AE100520	493	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10058	Intron10	0	XPNPEP2-X15a	CTTGTGAACTTACAGAAAGTC	AE10058	430	AGAGAGGAAAGTACTCCACA	AE100520	494
Aminopeptidase P (membrane bound)	XPNPEP2	AE10059	Intron10	0	XPNPEP2-X15a	AE10059	431	AGAGAGGAAAGTACTCCACA	AE100520	495	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10060	Intron17	0	XPNPEP2-X15a	GGAAAGGAAACCAAGATTTAC	AE10060	432	TAAAGAGGAGCCGGATGATGAG	AE100520	496
Aminopeptidase P (membrane bound)	XPNPEP2	AE10061	Intron13	0	XPNPEP2-X15a	AGTAGAGGTTGAGGAGGSC	AE10061	433	GCAGTCCTACCTCACACATG	AE100520	497
Aminopeptidase P (membrane bound)	XPNPEP2	AE10062	Intron12	0	XPNPEP2-X15a	AE10062	434	GCAGTCCTACCTCACACATG	AE100520	498	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10063	Intron13	0	XPNPEP2-X15a	AE10063	435	AGAGTGAGACGCTGCCTCC	AE100520	499	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10064	Exon1	0	XPNPEP2-X15a	AE10064	436	GCAGTCCTACCTCACACATG	AE100520	500	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10065	Intron8	0	XPNPEP2-X15a	AE10065	437	CTTACCCCTAGTAGGCCCTCC	AE100520	501	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10066	Intron17	0	XPNPEP2-X15a	AGGGTTCTGGCTCTTGGAA	AE10066	438	AGCTGGATCTGGATGGATGAA	AE100520	502
Aminopeptidase P (membrane bound)	XPNPEP2	AE10067	Intron8	0	XPNPEP2-X15a	AE10067	439	AGCTGGATCTGGATGGATGAA	AE100520	503	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10068	Intron15	0	XPNPEP2-X15a	AE10068	440	AGCTGGATCTGGATGGATGAA	AE100520	504	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10069	Intron20	0	XPNPEP2-X15a	AE10069	441	TGGGACCTCTCCATAGGCTCT	AE100520	505	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10070	Intron21	0	XPNPEP2-X15a	AE10070	442	TGGGACCTCTCCATAGGCTCT	AE100520	506	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10071	Exon21	0	XPNPEP2-X15a	AE10071	443	GGTTGATGTTCTCCATGCTCT	AE100520	507	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10072	Exon21	0	XPNPEP2-X15a	AE10072	444	GGTTGATGTTCTCCATGCTCT	AE100520	508	
Aminopeptidase P (membrane bound)	XPNPEP2	AE10073	Exon21	0	XPNPEP2-X15a	AE10073	445	TGGGACCTCTCCATGCTCT	AE100520	509	
Burkittin Receptor B1	BDKRB1	AE10241	Exon1	0	BDKRB1-X15a	AE10241	446	TGGGACCTCTCCATGCTCT	AE100520	510	
Burkittin Receptor B1	BDKRB1	AE10242	Exon2	0	BDKRB1-X15a	AE10242	447	ATGGAGCTTCTGGCTGGATGAA	AE100520	511	
Burkittin Receptor B1	BDKRB1	AE10243	Exon3	0	BDKRB1-X15a	AE10243	448	AGGGACATCTCTGGAGAGG	AE100520	512	
Burkittin Receptor B1	BDKRB1	AE10244	Exon3	0	BDKRB1-X15a	AE10244	449	TGGGTTGTTCTCTTCTCTCT	AE100520	513	
Burkittin Receptor B2	BDKRB2	AE10245	Intron1	1	BDKRB2-X15a	AE10245	450	CTTGGATGTTCTCTTCTCT	AE100520	514	
Burkittin Receptor B2	BDKRB2	AE10246	Intron1	1	BDKRB2-X15a	AE10246	451	CTTGGGTTCTCTCTCTCT	AE100520	515	
Burkittin Receptor B2	BDKRB2	AE10247	Intron1	1	BDKRB2-X15a	AE10247	452	CGGGAGGAACTTCTCTCT	AE100520	516	
Burkittin Receptor B2	BDKRB2	AE10248	Intron1	1	BDKRB2-X15a	AE10248	453	CGGGAGGAACTTCTCTCT	AE100520	517	
Burkittin Receptor B2	BDKRB2	AE10249	Intron1	1	BDKRB2-X15a	AE10249	454	CGGGAGGAACTTCTCTCT	AE100520	518	
Burkittin Receptor B2	BDKRB2	AE10250	Exon2	0	BDKRB2-X15a	AE10250	455	CGGGAGGAACTTCTCTCT	AE100520	519	
Burkittin Receptor B2	BDKRB2	AE10251	Exon3	0	BDKRB2-X15a	AE10251	456	CGGGAGGAACTTCTCTCT	AE100520	520	
Burkittin Receptor B2	BDKRB2	AE10252	Exon3	0	BDKRB2-X15a	AE10252	457	GGTGGAGAGAACAGCTGAA	AE100520	521	
Burkittin Receptor B2	BDKRB2	AE10253	Exon3	0	BDKRB2-X15a	AE10253	458	GGAGAGAGGAACTTCTCTCT	AE100520	522	
Burkittin Receptor B2	BDKRB2	AE10254	Exon3	0	BDKRB2-X15a	AE10254	459	GGAGAGAGGAACTTCTCTCT	AE100520	523	
Burkittin Receptor B2	BDKRB2	AE10255	Exon3	0	BDKRB2-X15a	AE10255	460	GGAGAGAGGAACTTCTCTCT	AE100520	524	
Burkittin Receptor B2	BDKRB2	AE10256	Exon3	0	BDKRB2-X15a	AE10256	461	GGAGAGAGGAACTTCTCTCT	AE100520	525	
Burkittin Receptor B2	BDKRB2	AE10257	Exon3	0	BDKRB2-X15a	AE10257	462	GGAGAGAGGAACTTCTCTCT	AE100520	526	
Burkittin Receptor B2	BDKRB2	AE10258	Exon3	0	BDKRB2-X15a	AE10258	463	GGAGAGAGGAACTTCTCTCT	AE100520	527	
Burkittin Receptor B2	BDKRB2	AE10259	Exon3	0	BDKRB2-X15a	AE10259	464	GGAGAGAGGAACTTCTCTCT	AE100520	528	
Burkittin Receptor B2	BDKRB2	AE10260	Exon3	0	BDKRB2-X15a	AE10260	465	GGAGAGAGGAACTTCTCTCT	AE100520	529	
Tachykin Receptor 1	TACR1	AE10852	Exon2	1	TACR1-X2a	GAAGAAGGAACTTCTCTCT	AE10852	466	TGACGAGAAAAGATGGATGCT	AE108520	531
Tachykin Receptor 1	TACR1	AE10853	Intron3	1	TACR1-X2a	AE10853	467	TGACGAGAAAAGATGGATGCT	AE108520	532	
Tachykin Receptor 1	TACR1	AE10854	Exon3	1	TACR1-X2a	AE10854	468	TGACGAGAAAAGATGGATGCT	AE108520	533	
Tachykin Receptor 1	TACR1	AE10855	Exon3	1	TACR1-X2a	AE10855	469	TGACGAGAAAAGATGGATGCT	AE108520	534	
Tachykin Receptor 1	TACR1	AE10856	Exon3	1	TACR1-X2a	AE10856	470	TGACGAGAAAAGATGGATGCT	AE108520	535	
Tachykin Receptor 1	TACR1	AE10857	Exon3	1	TACR1-X2a	AE10857	471	TGACGAGAAAAGATGGATGCT	AE108520	536	
Tachykin Receptor 1	TACR1	AE10858	Exon3	1	TACR1-X2a	AE10858	472	TGACGAGAAAAGATGGATGCT	AE108520	537	
Tachykin Receptor 1	TACR1	AE10859	Exon3	1	TACR1-X2a	AE10859	473	TGACGAGAAAAGATGGATGCT	AE108520	538	
Tachykin Receptor 1	TACR1	AE10860	Exon3	1	TACR1-X2a	AE10860	474	TGACGAGAAAAGATGGATGCT	AE108520	539	
Tachykin Receptor 1	TACR1	AE10861	Exon3	1	TACR1-X2a	AE10861	475	TGACGAGAAAAGATGGATGCT	AE108520	540	
Tachykin Receptor 1	TACR1	AE10862	Exon3	1	TACR1-X2a	AE10862	476	TGACGAGAAAAGATGGATGCT	AE108520	541	
Tachykin Receptor 1	TACR1	AE10863	Exon3	1	TACR1-X2a	AE10863	477	TGACGAGAAAAGATGGATGCT	AE108520	542	
Tachykin Receptor 1	TACR1	AE10864	Exon3	1	TACR1-X2a	AE10864	478	TGACGAGAAAAGATGGATGCT	AE108520	543	
Tachykin Receptor 1	TACR1	AE10865	Exon3	1	TACR1-X2a	AE10865	479	TGACGAGAAAAGATGGATGCT	AE108520	544	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0734	Intron3	0	KLK1-X2a	CGTACAGAGGAACTTCTCTCT	AE0734	480	TCTGACACAGAGCTGTCTT	AE107340	545
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0735	Intron3	0	KLK1-X2a	AE0735	481	TCTGACACAGAGCTGTCTT	AE107340	546	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0736	3' Flank	0	KLK1-X2a	AE0736	482	TCTGACACAGAGCTGTCTT	AE107340	547	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0737	Exon3	0	KLK1-X2a	AE0737	483	TCTGACACAGAGCTGTCTT	AE107340	548	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0738	Exon3	0	KLK1-X2a	AE0738	484	TCTGACACAGAGCTGTCTT	AE107340	549	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0739	Exon3	0	KLK1-X2a	AE0739	485	TCTGACACAGAGCTGTCTT	AE107340	550	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0740	Exon3	0	KLK1-X2a	AE0740	486	TCTGACACAGAGCTGTCTT	AE107340	551	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0741	Exon3	0	KLK1-X2a	AE0741	487	TCTGACACAGAGCTGTCTT	AE107340	552	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0742	3' Flank	0	KLK1-X2a	AE0742	488	TCTGACACAGAGCTGTCTT	AE107340	553	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0743	Exon3	0	KLK1-X2a	AE0743	489	TCTGACACAGAGCTGTCTT	AE107340	554	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0744	Exon3	0	KLK1-X2a	AE0744	490	TCTGACACAGAGCTGTCTT	AE107340	555	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0745	Exon3	0	KLK1-X2a	AE0745	491	TCTGACACAGAGCTGTCTT	AE107340	556	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0746	Exon3	0	KLK1-X2a	AE0746	492	TCTGACACAGAGCTGTCTT	AE107340	557	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0747	Exon3	0	KLK1-X2a	AE0747	493	TCTGACACAGAGCTGTCTT	AE107340	558	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0748	Exon3	0	KLK1-X2a	AE0748	494	TCTGACACAGAGCTGTCTT	AE107340	559	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0749	Exon3	0	KLK1-X2a	AE0749	495	TCTGACACAGAGCTGTCTT	AE107340	560	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0750	Exon3	0	KLK1-X2a	AE0750	496	TCTGACACAGAGCTGTCTT	AE107340	561	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0751	Exon3	0	KLK1-X2a	AE0751	497	TCTGACACAGAGCTGTCTT	AE107340	562	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0752	Exon3	0	KLK1-X2a	AE0752	498	TCTGACACAGAGCTGTCTT	AE107340	563	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0753	Exon3	0	KLK1-X2a	AE0753	499	TCTGACACAGAGCTGTCTT	AE107340	564	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0754	Exon3	0	KLK1-X2a	AE0754	500	TCTGACACAGAGCTGTCTT	AE107340	565	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0755	Exon3	0	KLK1-X2a	AE0755	501	TCTGACACAGAGCTGTCTT	AE107340	566	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0756	3' Flank	0	KLK1-X2a	AE0756	502	TCTGACACAGAGCTGTCTT	AE107340	567	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0757	Exon3	0	KLK1-X2a	AE0757	503	TCTGACACAGAGCTGTCTT	AE107340	568	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0758	Exon3	0	KLK1-X2a	AE0758	504	TCTGACACAGAGCTGTCTT	AE107340	569	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0759	Exon3	0	KLK1-X2a	AE0759	505	TCTGACACAGAGCTGTCTT	AE107340	570	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0760	Exon3	0	KLK1-X2a	AE0760	506	TCTGACACAGAGCTGTCTT	AE107340	571	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0761	Exon3	0	KLK1-X2a	AE0761	507	TCTGACACAGAGCTGTCTT	AE107340	572	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0762	Exon3	0	KLK1-X2a	AE0762	508	TCTGACACAGAGCTGTCTT	AE107340	573	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0763	Exon3	0	KLK1-X2a	AE0763	509	TCTGACACAGAGCTGTCTT	AE107340	574	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0764	Exon3	0	KLK1-X2a	AE0764	510	TCTGACACAGAGCTGTCTT	AE107340	575	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0765	Exon3	0	KLK1-X2a	AE0765	511	TCTGACACAGAGCTGTCTT	AE107340	576	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0766	Exon3	0	KLK1-X2a	AE0766	512	TCTGACACAGAGCTGTCTT	AE107340	577	
Kalikrein 1 (renal/pancreas/salivary)	KLK1	AE0767	Exon3	0							

Table IX(2 of 2)

Bradykinin Receptor B2	BDKRB2	AE104628	Exon3	1	EDKRH2_X3-2a	TTCTGTAGAAGACAGACAGTC	AE104655	785	TATGCCAACATCTGCCC	AE104656	817
Bradykinin Receptor B2	BDKRB2	AE104629	Exon3	1	EDKRH2_X3-2a	TTCTGTAGAAGACAGACAGTC	AE104655	786	TATGCCAACATCTGCCC	AE104656	818
Arachidylidene Eicosanoate 2	ACE2	AE10931	Intron14	1	ACE2_X1a	TTTAAAGATGGACACATGGC	AE109327	—	AGTGATGCGGAGAAAGAAA	AE109328	819
Arachidylidene Eicosanoate 2	ACE2	AE10932	Intron12	1	ACE2_X1a	CAGCTTGATGACAGCTCTCA	AE109321	788	AGACAGAACGCGCTAAAG	AE109322	820
Arachidylidene Eicosanoate 2	ACE2	AE10933	Intron13	1	ACE2_X1a	CGAGCTTGATGACAGCTCTCA	AE109321	789	AGACAGAACGCGCTAAAG	AE109322	821
Arachidylidene Eicosanoate 2	ACE2	AE10934	Intron3	1	ACE2_X3a	TTATCATGTCCTGCCCTCA	AE109321	790	TCTTACGAAATACTTCATGTT	AE109322	822
Arachidylidene Eicosanoate 2	ACE2	AE10935	Intron2	1	ACE2_X3a	TTATCATGTCCTGCCCTCA	AE109321	791	TCTTACGAAATACTTCATGTT	AE109322	823
Arachidylidene Eicosanoate 2	ACE2	AE10936	Intron16	1	ACE2_X1a	GCACAGAGAGAGAACAGAACAA	AE109319	792	CTTGCCGACATGCTGTTGTT	AE109320	824
Arachidylidene Eicosanoate 2	ACE2	AE10937	Exon16	1	ACE2_X1a	GCACAGAGAGAGAACAGAACAA	AE109319	793	CTTGCCGACATGCTGTTGTT	AE109320	825
Protease inhibitor 4	P14	AE10931	Intron1	0	P14_X2a	GATGGGGGGGAGCTGTTGCTG	AE109323	794	CAACAGAGAGAGAACATGCG	AE109324	826
Protease inhibitor 4	P14	AE10932	Intron2	0	P14_X2a	GATGGGGGGAGCTGTTGCTG	AE109323	795	CAACAGAGAGAGAACATGCG	AE109324	827
Protease inhibitor 4	P14	AE10933	Intron13	0	P14_X2a	CTTTCACACGGGAGCTGGG	AE109322	796	ACTTGATGCGCTTACAGTTT	AE109323	828
Protease inhibitor 4	P14	AE10934	Intron2	0	P14_X2a	CTTTCACACGGGAGCTGGG	AE109322	797	ACTTGATGCGCTTACAGTTT	AE109323	829
Protease inhibitor 4	P14	AE10935	Exon11	0	P14_X1sa	CTTACCCCGGCTTCTCCG	AE109319	798	CGGTGTTGGAATTACGATA	AE109320	830
Protease inhibitor 4	P14	AE10936	Exon16	0	P14_X12a	TTGGGGGGGAGAACAGTGAT	AE109321	799	CCACAGAGAGAGAACATGAG	AE109322	831
Protease inhibitor 4	P14	AE10937	Exon17	0	P14_X12a	TTGGGGGGGAGAACAGTGAT	AE109321	800	TAATGAACTCTCCCAAAGATG	AE109322	832
Protease inhibitor 4	P14	AE10938	Exon18	0	P14_X11a	AAAAATAATGCTGGCTGTGCT	AE109323	801	TAATGAACTCTCCCAAAGATG	AE109324	833
Protease inhibitor 4	P14	AE10939	Exon19	0	P14_X11a	AAAAATAATGCTGGCTGTGCT	AE109323	802	TAATGAACTCTCCCAAAGATG	AE109324	834
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron11	0	XPNPEP2_X12a	ATTCCTTCTTGTGAGCTGCT	AE10947	1014	ACCAAGAACCTCTGCTCTCT	AE10948	1040
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron12	0	XPNPEP2_X13a	AGTTGAGGGTAGGGAGGCC	AE10951	1015	GGAACTCCCTACTCCAGACCTG	AE10952	1041
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron13	0	XPNPEP2_X13a	AGTTGAGGGTAGGGAGGCC	AE10951	1016	GGAACTCCCTACTCCAGACCTG	AE10952	1042
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron14	0	XPNPEP2_X13a	AGGGTGGCGCTGCTTGTAG	AE10951	1017	CTTACCCCTCTCTGCTGCG	AE10952	1043
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron15	0	XPNPEP2_X13a	CAAAAGCTGTAAACCTCCCA	AE10952	1018	CTGACCCCTCTCTGCTGCG	AE10955	1044
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron16	0	XPNPEP2_X13a	CAAAAGCTGTAAACCTCCCA	AE10952	1019	CTGACCCCTCTCTGCTGCG	AE10955	1045
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron17	0	XPNPEP2_X13a	ACATACCAAGCTGATGCCAC	AE10952	1020	GAAGGAACTGGCTGCGGAG	AE10956	1046
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron18	0	XPNPEP2_X13a	CTTACGGCTCTGCTGCTG	AE10952	1021	TGGCTGTTGCTGCTGCTG	AE10956	1047
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron19	0	XPNPEP2_X13a	CTTACGGCTCTGCTGCTG	AE10952	1022	TGGCTGTTGCTGCTGCTG	AE10956	1048
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron20	0	XPNPEP2_X13a	CTTACGGCTCTGCTGCTG	AE10952	1023	TGGCTGTTGCTGCTGCTG	AE10956	1049
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron21	0	XPNPEP2_X13a	CTTACGGCTCTGCTGCTG	AE10952	1024	TGGCTGTTGCTGCTGCTG	AE10956	1050
Anticardiolipase P (Intrinsic site bound)	XPNPEP2	AE10932	Intron22	0	XPNPEP2_X13a	CTTACGGCTCTGCTGCTG	AE10952	1025	TGGCTGTTGCTGCTGCTG	AE10956	1051
Bradykinin Receptor B1	BDKRB1	AE10930	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1026	TATGGACAAACCATCTGCCC	AE10956	1052
Bradykinin Receptor B1	BDKRB1	AE109310	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1027	GAGTCACGAACTGAAAT	AE10956	1053
Bradykinin Receptor B1	BDKRB1	AE109311	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1028	GAGTCACGAACTGAAAT	AE10956	1054
Bradykinin Receptor B1	BDKRB1	AE109312	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1029	GAGTCACGAACTGAAAT	AE10956	1055
Bradykinin Receptor B1	BDKRB1	AE109313	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1030	CTTCACCTCTTCCAGCG	AE10957	1056
Bradykinin Receptor B1	BDKRB1	AE109314	Exon3	0	BDKRB1_X21a	CTTACGGCTCTGCTGCTG	AE10952	1031	CTTCACCTCTTCCAGCG	AE10957	1057
Bradykinin Receptor B2	BDKRB2	AE109330	Exon3	1	BDKRB2_X21a	CTTACGGCTCTGCTGCTG	AE10952	1032	CAGGTGTTGAACTGCTG	AE10957	1058
Bradykinin Receptor B2	BDKRB2	AE109331	Exon3	1	BDKRB2_X21a	CTTACGGCTCTGCTGCTG	AE10952	1033	TATGGACAAACCATCTGCCC	AE10956	1059
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1034	TATGGACAAACCATCTGCCC	AE10956	1060
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1035	TATGGACAAACCATCTGCCC	AE10956	1061
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1036	TATGGACAAACCATCTGCCC	AE10956	1062
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1037	TATGGACAAACCATCTGCCC	AE10956	1063
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1038	TATGGACAAACCATCTGCCC	AE10956	1064
Bradykinin Receptor B2	BDKRB2	AE109332	Intron1	—	BDKRB2_X1a	CTTACGGCTCTGCTGCTG	AE10952	1039	TATGGACAAACCATCTGCCC	AE10956	1065
Tachykinin Receptor 1	TACH1	AE10938	Intron3	1	TACH1_X4a	TGTTCTGTTCTCTGCT	AE10951	1096	CITACCGTCGCAACCCCTG	AE10952	1092
Tachykinin Receptor 1	TACH1	AE10939	Intron13	1	TACH1_X4a	CCTCTCTCTCTGCTGCT	AE10951	1097	GlACGTCGCAACCCCTG	AE10952	1093
Arachidylidene Eicosanoate 2	ACE2	AE10938	Intron13	1	ACE2_X1a	CAAGCTGTGAGAACAGAGCA	AE10951	1098	ACATCGTCGCAACCCCTG	AE10952	1094
Arachidylidene Eicosanoate 2	ACE2	AE10939	Intron6	1	ACE2_X4a	TAAGCTGCTGCTGCTGCT	AE10951	1099	TCTTCGCTGGGGTTTCAATT	AE10952	1095

**Table X (1 of 3)**

SNP_ID	ORCHID LEFT (SEQ ID NO.:)	ORCHID RIGHT (SEQ ID NO.:)	ORCHID SNPIT (SEQ ID NO.:)	ORCHID SNPIT (SEQ ID NO.:)
AE100s1	TATCATTTGCCCCCTATCACCG	1066	CAGGGTCAGGGAAAGCC	1154
AE100s10	AACTCTCATTCAGAGTACCAAG	1067	GAGGCATTGTGATGACCTCC	1155
AE100s11	ATAGAATGACTTCCCTCCAGAGGA	1068	CAGCTAACCTGTGACTGGG	1156
AE100s12	TCCAGGGAGACTGCCCTG	1069	CAAGGGCCGCCCTAACCCCTG	1157
AE100s13	ATAGAATGACTTCCAGACCGA	1070	GCTGAGRAAGGGAGAATGTT	1158
AE100s14	N/A	N/A	N/A	N/A
AE100s15	ACCCCTCTGCGCAG	1071	GATGGAGGGAGGGAG	1159
AE100s16	AAGAGAGGGAGAAGAGGAA	1072	GTTGAGAATAGAGAAGGGTTATAGC	1160
AE100s17	N/A	N/A	N/A	N/A
AE100s18	AACACGAAAGACCCCTCTCA	1073	GATCCCAGACGACATCTATGAGC	1161
AE100s19	N/A	N/A	N/A	N/A
AE100s2	ATAGATTTGAGGGAGGG	1074	GTTATTTGCAAGTCAACTCCC	1162
AE100s20	TACACACAGGGAGTGC	1075	GATTCAGGTACTTGACCTCGG	1163
AE100s21	N/A	N/A	N/A	N/A
AE100s22	N/A	N/A	N/A	N/A
AE100s23	TTTGCTTAAGGACACACAAATT	1076	GAGGGGGGTCTAGGGACT	1164
AE100s24	CGCTANCTCATCCATCATCT	1077	CCGCACCTTGACTTGCGG	1165
AE100s25	N/A	N/A	N/A	N/A
AE100s26	N/A	N/A	N/A	N/A
AE100s27	ACAAGTAAGAGTTGTTGGAAAG	1078	GAGCCCCAAAAGTCTAATGTA	1166
AE100s28	N/A	N/A	N/A	N/A
AE100s29	N/A	N/A	N/A	N/A
AE100s3	N/A	N/A	N/A	N/A
AE100s30	TATCTTCTTCACTGTTGCACCA	1079	CAATGGACAGAGGAGGG	1167
AE100s4	TCCCTGCTGCTCCCGG	1080	AATATTGTTGCTGTTTACAGAATAG	1168
AE100s5	N/A	N/A	N/A	N/A
AE100s6	TGTGTCATGAGTTGATG	1081	CTTGTGTCATTCATCATCTGTAA	1169
AE100s7	ATCCAGTAATGCAAGGAG	1082	GTCAGCCCTAGGGTAACAGTTG	1170
AE100s8	GCAAANTCTACCTCTCTG	1083	CAGGTCTCGGGCCACAGTA	1171
AE100s9	AAACTAGAAAGAGAAGACAC	1084	TTCATAGGGACTGCCAGGAG	1172
AE103s1	AACTCTTCTCCCTACTACAGCT	1085	GATGAAATAATGGAGGAGCTTAG	1173
AE103s10	N/A	N/A	N/A	N/A
AE103s11	TGGACTTGATGATGTTACAAATT	1086	GACTCTGAGCTCCCTCCTC	1174
AE103s12	N/A	N/A	N/A	N/A
AE103s13	CCACCGACTTTCTGTTAATTG	1087	CTTTCATAATGAACTGATGTTAATAGCA	1175
AE103s14	TGTCTATACAGGAGGAGGA	1088	CCTGGCAGTTGCTGAGAAC	1176
AE103s15	TTGACATGTCAGAGGCC	1089	CAACAGGACAAAAAGCTTCC	1177
AE103s16	ACTTTTCGGCCAAATAACA	1090	ACCCCCCAATCTTGCGGA	1178
AE103s17	N/A	N/A	N/A	N/A
AE103s18	ATCTGAACATACCGCTT	1092	GTAATGTTGAGAGGAGTCGC	1180
AE103s9	N/A	N/A	N/A	N/A
AE104s1	GAGGCAATAATGTCGTTTGTAA	1093	CTTACCCCTGCTGCTGTG	1181
AE104s10	GGTGGGGCTCAGGGT	1094	GGGGGGTTGAGGACCC	1182

**Table X (2 of 3)**

SNP_ID	ORCHID LEFT (SEQ ID NO:)	ORCHID LEFT <sup>*</sup> (SEQ ID NO:)	ORCHID RIGHT (SEQ ID NO:)	ORCHID RIGHT <sup>*</sup> (SEQ ID NO:)	ORCHID SNPIT (SEQ ID NO:)
AE104s11	TGGGATGAAATGGCTCCCTG	1095	GCCCCATGCGCTAGATG	1183	TTACACATACACCCNATGAGCTT
AE104s12	ATTTCCTGGTTGATGTGATG	1096	CGGCCCTATGCATGCTGTA	1184	TAACGCTATGGAGCTTCAG
AE104s13	GCCATTGGCGAGACCTC	1097	AAAAAAAGGGCTGTTTGICA	1185	GGCACTCATCCACCCAGAGAC
AE104s14	AAGTGAAGAGCTCCCT	1098	AAAGTGCGCCAGATGAGAC	1186	CCCTAGAGAGTGAAAGGAATG
AE104s15	GATCGATGATGAGGGAGG	1099	CAGTATGGGAATTCATPATCC	1187	ATTCCTGACTCATTTAAACAAA
AE104s16	GATGAAACAGATGAGGGAGG	1100	CATAAATGCGCCATGCTCAT	1188	TAGCTTGAGCGGAGACSCCCAGGT
AE104s17	AGAGAAAAGGGTAGATGGCA	1101	CATTTGAGCTGGGAGATCACCA	1189	ACAGGGCTGGGGATNGCNAATAACAC
AE104s18	TAACATGAACTGAGACCCCTT	1102	CACTTGAGTCCAATGTTCTC	1190	GTTGTTGGCAGGGATGTCCTAC
AE104s19	GAGAGCAAATGGTGTGTTGATIA	1103	CTTCACCTGTGTTGTTG	1191	GTCAGGGAGGGCNACCTGGCGCG
AE104s20	TTAACATCCTCCAGGGCTGAG	1104	CTTCATCCAGATGCTACTGG	1192	TTTTTGAGCCCTTAAACCCCTTCCTTC
AE104s21	GGTTTCTTGTGAGCACTAC	1105	CATAACATTCGAGAAAGG	1193	GCAGAACCTGCTCTTTCTGGT
AE104s22	N/A	N/A	N/A	N/A	N/A
AE104s23	AGAGCTGGCTGGCGCG	1106	GAAGGAGGCGAGAGCTAG	1194	GAAGTGGCCAGGGCGTGTGACATCA
AE104s24	N/A	N/A	N/A	N/A	N/A
AE104s25	N/A	N/A	N/A	N/A	N/A
AE104s26	TGATAGATTAAGAAACCCAGG	1107	GTTTCCTGGTCCCAGGCC	1195	CATGCAACAAANCTGGATGC
AE104s27	TGACACGTCTCTCGAAC	1108	GAAGAGAGGAGCCTCTCCA	1196	GCTTTCNGTGTGTCAGTCGCACTC
AE104s28	N/A	N/A	N/A	N/A	N/A
AE104s29	N/A	N/A	N/A	N/A	N/A
AE104s30	TTCGCAAGGGAGGAAATC	1109	CAACCCCTGCACTCCAGC	1197	GAGGGAAGGGCTGCGCTCAGTCATCG
AE104s31	N/A	N/A	N/A	N/A	N/A
AE104s32	N/A	N/A	N/A	N/A	N/A
AE104s33	TAGGATACATGGCTAGGGCT	1110	GTTCGGGACCCATGTTCPAT	1198	ACCTTTGCTGATTTCACCTTA
AE104s34	ACACTGCGCPTCACCC	1111	GTACATGGGGATCWTAGCC	1199	GCTCTCCAAATCTGATTCGTC
AE104s35	N/A	N/A	N/A	N/A	N/A
AE104s36	CCCTTCGCTGTCATATCA	1112	CATCTGGAGGAACTCAAGCTCA	1200	ACCCACAGCACCCCTGACCGTTC
AE104s4	AGCTGAGGGCTGAGTCGA	1113	CTTGATGAAAGAGAGAGCA	1201	AGGTGGAGGAGGAGCTGGAGG
AE104s5	TGAGGGTTGCAAGGAGA	1114	CAAGAGGGCTCCCGCA	1202	GTGCGAGGAGCYCAGGCTGCT
AE104s6	GGCTCACAACTGGCAATTC	1115	CAAAAGAGGCTCCCGCA	1203	GTTTCCTGGAGAAAACCTTGCTG
AE104s7	AACCTGGCGCAGGGT	1116	AACCCCTTAACCAACCC	1204	CCCCCTCTCAAGCTTNTGTCACAA
AE104s8	ATGTCATGACGCCCTTGTCT	1117	GGAGACCAAGTTCTAGTC	1205	GAAGGGAAACTGAGGAGGACAG
AE104s9	TATTTCTAGCCAGCTCTTCTTATAG	1118	GAAGCTGGCTGAGGTMAAGG	1206	AAGGGCTACTTANTGAGGCTC
AE105s1	GAGAGACCTGAGGGCG	1119	AGCTCTTACCTGGCTCTCA	1207	CCAGCGCTGGGAGAAGAGA
AE105s2	ATTGTCACAGGGTGGCG	1120	CAAACTCAGATGTTGGAGACG	1208	GAGTGGCGTGGAGAAGCTGTTAG
AE105s3	N/A	N/A	N/A	N/A	N/A
AE105s4	GCGAAAGGAGGCGCA	1121	TTCAGTGGTGTGCGCAA	1209	AGCGTGAANCTCTAGATGGSTCA
AE105s5	TGTTGGGGGAGCTTGG	1122	GTGTCGATGGGGAAAGG	1210	AGGCTTACACCGCTCTCTAG
AE105s6	ATTCCTGCTGCCCAAC	1123	CATACTGCGCCATGAGAC	1211	GGAACTTCTGCTTCAGAGCA
AE106s1	TATCAAGGCCCCAGCG	1124	CAACAGAAATGTTACAGGC	1212	TACCTGGCAAGACGCCGATGG
AE106s2	ATGGCTCTGGTGGTGAATAGC	1125	CTTCATACATACCTCCAGC	1213	CGAGGAGGAGGAGGACACCA
AE106s3	ATGACCGGGATGGCTG	1126	CTAACACAGGAAATGCTG	1214	CCAGCGCAAGTGAAGGAGG
AE106s4	TGCAAGATTCATGAGAATGA	1127	CTGPKTACTCAACAAATCCT	1215	AGGTGGACCCANCMTTCCCA
AE106s5	AAAAGCTGTCGACPTTATT	1128	TCAAATAATCTCATCTTCT	1216	TCCCTATCTTGGNACNCTNATGCT
AE106s6	TTCAGCTCAMACCGCTGAG	1129	CATGCAAATTCCTCTCATCTG	1217	ACCCATACAGGACCTTITGCAAGTC
AE106s7	ATGGCTCTGGACTCTGCTG	1130	CCCAAGGAGGAGGAGCAG	1218	AGGCACTINGAGGCTAGTCAAGGA

**Table X (3 of 3)**

SNP_ID	ORCHID LEFT	SEQ ID NO:)	ORCHID RIGHT	(SEQ ID NO:)	ORCHID_SNPIT (SEQ ID NO:)
AE106s8	N/A	N/A	N/A	N/A	N/A
AE106s9	N/A	N/A	N/A	N/A	N/A
AE107s1	GTCGTAGTCATTCCAGATGTC	1131	ACACACAGCATGAACTGTCAC	1219	CAAAATCCTGCCTPAATGATGATC
AE107s2	ACCATGAAACCAGAGAATTTATG	1132	CCTCCCTTGCCCTTTC	1220	TCCCTTGACRCAAGGATGCCATCCC
AE107s3	CCTGCTGATCACACAGAATG	1133	CATACAATTCTCTGGTGTGATGC	1221	GCTGTAAGCTGAGTAGTGGCAGC
AE107s4	ATCGAACCGAGAATGTTATGTCG	1134	GGGAGAAAAAGGGTGA	1222	AAGGCGGGATGGGACTCTCTG
AE107s5	ACCTGGAAACCATTCGCTCC	1135	CCTPTCCACCCACCTCCTG	1223	TONGCCACACCCACACTTGTCGA
AE107s6	CCAGTAAATAACAAATGCTCC	1136	CAGCTCAAGCCGAGTGCG	1224	ATGTTGTCAGTTGCTGCCATCACC
AE109s1	AATAGCTTACCAATAGGATAGTTT	1137	GAATTGATTAATTGGTCAAGTC	1225	ATCTSGAACTTATACATTGAAAGAA
AE109s2	GGGGGGTCAAGGGCTTT	1138	GCAAAATTAGCCAACTGAAAGAGA	1226	GAGGGTTCCAGAACTAAATTTA
AE109s3	TGGGCCAAAGGAGACTG	1139	GCTGAAAGCAGAAAGAGAATTC	1227	AGTAGAAAGGAAAGGTTGAA
AE109s4	GTGTTGAAAACACACATATCTCAAT	1140	TGAAAAAGTTGTTACCAAGATAATC	1228	TCATATCACNANTAAANTPAAGTAC
AE109s5	GTGTCACACTGCACATAAAATAAAC	1141	ACATGCCAAAGGAAATTTGCTG	1229	GAATTGTTGCTGAAAGAAATCTAA
AE109s6	AACTCAAACTCAACACATAACGATT	1142	GTTTACCAATACACACATAACGATT	1230	CACATGAAATGACTCAGAAATATC
AE109s7	CCCTCACCCCTTAGTAAAGTAAA	1143	TTTCGAAACCAAGATACTCTTTATT	1231	TTCAGTTCTAGGAATATATCAGACAC
AE109s8	N/A	N/A	N/A	N/A	N/A
AE109s9	AGGCCTCACTCAAAANGCCATT	1144	TGCCCTCCCTGCTCATTTG	1232	CTTGTTAAANAAACCCATNAAATCTTC
AE110s1	N/A	N/A	N/A	N/A	N/A
AE110s10	CACCTGGAGCTGGATGAG	1145	ATCTGGGATGGTGGCTGG	1233	GTTGGCACCCGGGTTGGCAGGCCAC
AE110s11	CACCCRCGCAACCTCA	1146	CATGGTGTCACTTCAGAAATTG	1234	AACCTTCGGGCAAGGGCTGAAACA
AE110s12	AGATTGGGAGAAACTGG	1147	CACTGAACTGGTCTTGTATGTPACC	1235	TNTCTGGACACATGTTWATTGAA
AE110s2	CTGTRACCTCTTTCATTCCTT	1148	CCACACATCGGGACCC	1236	CCGGACTGTTGTTCTCATCACACATA
AE110s3	AAGGAGGGCTGCCAG	1149	GATGCAACTCTGCTTGTAAAAATT	1237	GATCTGGCTGTTCTCATANTCTAATG
AE110s4	N/A	N/A	N/A	N/A	N/A
AE110s5	CTTATCACGACCACTCAAA	1150	GATTAACTATACCAAGTGTGACTT	1238	GAGGGAAAGATTTGGATTTGGTCAG
AE110s6	GTCAAACAACTAAATGGCTGAA	1151	TTTCGAGTGGTGTGATTTGATGTC	1239	AGACCCCTAAATAAACCTCTGGGAT
AE110s7	AGGTCAAACTAAATGGCTGAA	1152	CACTGTCCTTCACATGACTGTTTC	1240	TAACCCATATAAGGACTCCACAGA
AE110s8	AGAAACTGGAGPATCCGTCGGA	1153	CTCTGAACTGAGTCAACTGCTTGT	1241	TATGAAACGTCAGTAACTGTTCTATCCCC
AE110s9	N/A	N/A	N/A	N/A	N/A

Table XI (1 of 3)

SNP_ID	GBS_LEFT (SEQ ID NO.)	GBS_RIGHT (SEQ ID NO.)
AE100s1	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1330
AE100s10	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1331
AE100s11	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1332
AE100s12	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1333
AE100s13	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1334
AE100s14	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1335
AE100s15	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1336
AE100s16	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1337
AE100s17	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1338
AE100s18	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1339
AE100s19	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1340
AE100s2	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1341
AE100s10	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1342
AE100s21	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1343
AE100s22	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1344
AE100s23	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1345
AE100s24	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1346
AE100s25	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1347
AE100s26	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1348
AE100s27	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1349
AE100s28	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1350
AE100s29	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1351
AE100s3	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1352
AE100s30	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1353
AE100s21	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1354
AE100s4	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1355
AE100s5	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1356
AE100s6	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1357
AE100s7	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1358
AE100s8	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1359
AE100s9	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1360
AE100s16	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1361
AE100s10	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1362
AE100s11	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1363
AE100s12	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1364
AE100s13	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1365
AE100s14	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1366
AE100s15	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1367
AE100s16	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1368
AE100s17	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1369
AE100s18	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1370
AE100s19	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1371
AE100s20	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1372
AE100s21	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1373
AE100s22	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1374
AE100s23	TCTAAACGAGCCCACTAATCTCCCTCCTTCACT	1375

**Table XI (2 of 3)**

SNP_ID	GBS_LEFT (SEQ ID NO.:)	GBS_RIGHT		GBS_RIGHT (SEQ ID NO.)
		GBS_LEFT (SEQ ID NO.:)	GBS_RIGHT (SEQ ID NO.:)	
AE104s11	TGTAAAACGACGGCCAGTTCGGGAGTTGAAATCT	1376	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1497
AE104s12	TGTAAAACGACGGCCAGTGCCTATCCTAAACCTCATCA	1377	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1498
AE104s13	TGTAAAACGACGGCCAGTCACTACCCATAGGGC	1378	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1499
AE104s14	TGTAAAACGACGGCCAGTCCATGGTCTCACTGGCC	1379	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1500
AE104s15	TGTAAAACGACGGCCAGTATAAACAGGTGTCGACCC	1380	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1501
AE104s17	TGTAAAACGACGGCCAGTCACTGGTCACTTAT	1381	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1502
AE104s18	TGTAAAACGACGGCCAGTCACTGGTCACTCACC	1382	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1503
AE104s19	TGTAAAACGACGGCCAGTGGAAATCCCTGACTCCC	1383	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1504
AE104s2	TGTAAAACGACGGCCAGTGGTCTTAAAGCGGCCCTG	1384	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1505
AE104s20	TGTAAAACGACGGCCAGTATAAACAGGTGTCGACCC	1385	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1506
AE104s21	TGTAAAACGACGGCCAGTCACTGGTCACTAACGTGGC	1386	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1507
AE104s22	TGTAAAACGACGGCCAGTGGAAATCCCTGAAATAAT	1387	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1508
AE104s23	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTGAC	1388	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1509
AE104s24	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1389	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1510
AE104s25	TGTAAAACGACGGCCAGTGGTCACTGGTCACTGGC	1390	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1511
AE104s26	TGTAAAACGACGGCCAGTGGTCACTGGTCACTGGC	1391	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1512
AE104s27	TGTAAAACGACGGCCAGTGGTCACTGGTCACTGGT	1392	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1513
AE104s28	TGTAAAACGACGGCCAGTGGTCTTCAATGGTCTGTG	1393	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1514
AE104s29	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1394	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1515
AE104s3	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1395	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1516
AE104s30	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1396	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1517
AE104s31	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1397	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1518
AE104s32	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1398	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1519
AE104s33	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1399	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1520
AE104s34	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1400	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1521
AE104s35	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1401	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1522
AE104s36	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1402	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1523
AE104s4	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1403	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1524
AE104s5	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1404	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1525
AE104s6	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1405	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1526
AE104s7	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1406	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1527
AE104s8	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1407	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1528
AE104s9	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1408	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1529
AE104s1	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1409	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1530
AE104s2	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1410	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1531
AE104s3	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1411	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1532
AE104s4	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1412	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1533
AE104s5	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1413	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1534
AE104s6	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1414	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1535
AE104s1	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1415	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1536
AE104s2	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1416	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1537
AE104s3	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1417	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1538
AE104s4	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1418	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1539
AE104s5	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1419	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1540
AE104s6	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1420	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1541
AE104s7	TGTAAAACGACGGCCAGTGGTCTTCACTGGCTGTG	1421	CAGGAAACGCTTATGCCAGCGCTTGTTCTCACACA	1542

**Table XI (3 of 3)**

SNP_ID	GBS_LEFT (SEQ_ID NO.)	GBS_LEFT (SEQ_ID NO.)	GBS_RIGHT (SEQ_ID NO.)	
AE10658	TGTAACAGGGCCACTAATGATTTCGGTTCCTTGT	1422	CAGGAACAGTGTGTTCCCTCCTGCCTACAT	1543
AE10659	TGTAACAGGGCCACTTAAAGCCAAAGTCG	1423	CAGGAACAGTGTGTTCCCTCCTGCCTACAT	1544
AE10751	TGTAACAGGGCCACTAATTTCATGGCCAGACT	1424	CAGGAACAGTGTGTTCCCTCCTGCCTACAT	1545
AE10752	TGTAACAGGGCCACTTGACAGGCTGCTGATA	1425	CAGGAACAGTGTGTTCAAGAGATGGCTGCGTAG	1546
AE10753	TGTAACAGGGCCACTCCAGTGCTGCTGATA	1426	CAGGAACAGTGTGTTCAAGAGATGGCTGCGTAG	1547
AE10754	TGTAACAGGGCCACTCCAGTGCTGCTGATA	1427	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1548
AE10755	TGTAACAGGGCCACTCTACCCCATAAATCAA	1428	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1549
AE10756	TGTAACAGGGCCACTTGACAGTGCTGCTTAT	1429	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1550
AE10951	TGTAACAGGGCCACTTGACAGTGCTAATGAAAGA	1430	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1551
AE10952	TGTAACAGGGCCACTTGACAGTGCTGCTGCG	1431	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1552
AE10953	TGTAACAGGGCCACTTAATGCGACCTCACATAG	1432	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1553
AE10954	TGTAACAGGGCCACTTTGACGAAATAAACCTGA	1433	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1554
AE10955	TGTAACAGGGCCACTTGACGTTGTTATCTGG	1434	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1555
AE10956	TGTAACAGGGCCACTTGCCATAGTGTAATGCC	1435	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1556
AE10957	TGTAACAGGGCCACTTGACAGAAACACAA	1436	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1557
AE10958	TGTAACAGGGCCACTTGACGATGCTGCTGTT	1437	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1558
AE10959	TGTAACAGGGCCACTTGCTTGCAAAANGGCAATTCT	1438	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1559
AE11051	TGTAACAGGGCCACTTGCTTGCTGTTGAAT	1439	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1560
AE11050	TGTAACAGGGCCACTTGCTGTTTCCTCAGA	1440	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1561
AE110511	TGTAACAGGGCCACTTGACATCTTCTCCCG	1441	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1562
AE110512	TGTAACAGGGCCACTTGAGGCTATGGAGTGATTA	1442	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1563
AE11052	TGTAACAGGGCCACTTGCTGACGCTGTTCTG	1443	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1564
AE11053	TGTAACAGGGCCACTTGCTTAACTCAATTGGG	1444	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1565
AE11054	TGTAACAGGGCCACTTGCTTAACTCTGAG	1445	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1566
AE11055	TGTAACAGGGCCACTTCTGCAAAATTCTGAAAGA	1446	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1567
AE11056	TGTAACAGGGCCACTTCTGCTCTAGGGTAAACA	1447	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1568
AE11057	TGTAACAGGGCCACTAAGGTTACATTCTATCC	1448	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1569
AE11058	TGTAACAGGGCCACTGATTGAGTGAAGCC	1449	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1570
AE11059	TCTAAACAGGGCCAGTGAACGGTCAATGCCATG	1450	CAGGAACAGTGTGTTCAACAACTCTGACCTTGAGG	1571

**Table XII**  
**Sample Description**

Race	Cases			Controls			Total
	Angioedema	Angioedema-like	Total	Angioedema	Angioedema-like	Total	
Blacks	11	10	21	32	19	51	72
Caucasians	12	22	34	38	69	107	141
Other	0	1	1	0	1	1	2
Total	23	33	56	70	89	159	215

**Table XIII**  
**Candidate Angioedema Susceptibility Genes**

Chromosome	Gene	Gene ID
14	Bradykinin B2 Receptor	BDKRB2
19	Tissue Kallikrein	KLK1
X	Aminopeptidase P (Membrane Bound)	XPNPEP2

**Table XIV**  
**Association of SNPs of the present invention with Angioedema and/or Angioedema-like Events**

Gene ID	SNP ID	Sample or Subgroup Scores Test		Estimate	Type	A,a <sup>1</sup>	Rare Allele	Copies of		OR	OR
		DF	Probability					(OR) <sup>2</sup>	Lower 95% CL		
BDKRB2	AE104s9	Caucasians	7.01	2	0.0300	Asymptotic	A,T	1	3.41	1.3238	8.7969
				0.0251		Exact			3.37	1.2261	10.2718
KLK1	AE107s2	Blacks	7.50	2	0.0062	Asymptotic	C,T	1	5.64	1.4211	22.3807
				0.0062		Exact			5.64	1.2422	34.7611
XPNPEP2	AE100s4	Caucasians	13.44	2	0.0009	Exact	C,T	2	14.95	1.9838	+INF
		Angioedema-like	11.39	2	0.0022	Exact		2	10.82	1.3105	+INF
		Overall	10.72	2	0.0047	Asymptotic		2	11.11	1.2687	97.2709

1 Most frequent (common) allele, least frequent (rare) allele.

2 The ratio of the odds of an adverse event (angioedema and/or Angioedema-like) in subjects carrying the specified number of copies of the rare allele, relative to controls matched for nationality, race, gender and starting dose, over the odds of such an adverse event for similarly matched subjects not carrying any copies of the rare allele.

3 Rare allele relative frequency.